GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2002, 21:57:21 ; Search time 2544.74 Seconds
(without alignments)
11584.861 Million cell updates/sec

Title: US-09-925-139-3
Perfect score: 1787
Sequence: 1 gtgaatctctggggccagga.....ggcattaaagtgctgtatcc 1787

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
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34: em_htg_inv:*
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36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1		46	2.6	46	6	AR032477	AR032477 Sequence
2		46	2.6	46	6	I29217	I29217 Sequence 89
3		46	2.6	46	6	I90891	I90891 Sequence 89
	c 4	21	1.2	24	6	AX020418	AX020418 Sequence
5		16	0.9	20	6	AR042917	AR042917 Sequence
6		16	0.9	20	6	AR073289	AR073289 Sequence
7		16	0.9	36	6	AX112428	AX112428 Sequence
8		15	0.8	22	4	DOG2155P01	L78641 Canis famil
	c 9	15	0.8	22	6	AR130748	AR130748 Sequence
10		15	0.8	25	6	E04451	E04451 DNA encodin
11		15	0.8	27	6	AR109648	AR109648 Sequence
	c 12	15	0.8	32	6	AX112429	AX112429 Sequence
13		15	0.8	41	6	A48824	A48824 Sequence 16
	c 14	14	0.8	20	6	AX167117	AX167117 Sequence
15		14	0.8	21	6	AR069484	AR069484 Sequence
16		14	0.8	22	6	AX146446	AX146446 Sequence
	c 17	14	0.8	22	6	AX146447	AX146447 Sequence
	c 18	14	0.8	23	6	A84872	A84872 Sequence 21
	c 19	14	0.8	23	6	AX077382	AX077382 Sequence
	c 20	14	0.8	23	6	AX148006	AX148006 Sequence
	c 21	14	0.8	25	6	AR130317	AR130317 Sequence
	c 22	14	0.8	25	6	AR130321	AR130321 Sequence
	c 23	14	0.8	26	6	AR090227	AR090227 Sequence
24		14	0.8	26	6	AR091212	AR091212 Sequence
	c 25	14	0.8	26	6	AX037841	AX037841 Sequence
26		14	0.8	27	6	A91913	A91913 Sequence 1
27		14	0.8	27	6	AR026695	AR026695 Sequence
	c 28	14	0.8	27	6	AR026699	AR026699 Sequence
29		14	0.8	27	6	AR026713	AR026713 Sequence
30		14	0.8	27	6	AR026714	AR026714 Sequence
31		14	0.8	27	6	AR029305	AR029305 Sequence
32		14	0.8	27	6	AR049121	AR049121 Sequence
	c 33	14	0.8	27	6	AR049125	AR049125 Sequence
34		14	0.8	27	6	AR049139	AR049139 Sequence
35		14	0.8	27	6	AR049140	AR049140 Sequence
36		14	0.8	27	6	AR065379	AR065379 Sequence
	c 37	14	0.8	27	6	AR065383	AR065383 Sequence
38		14	0.8	27	6	AR065397	AR065397 Sequence
39		14	0.8	27	6	AR065398	AR065398 Sequence
	c 40	14	0.8	28	6	I22030	I22030 Sequence 4
	c 41	14	0.8	31	6	AX167972	AX167972 Sequence
42		14	0.8	32	6	AX107235	AX107235 Sequence
43		14	0.8	32	6	AX107358	AX107358 Sequence
	c 44	14	0.8	33	6	AR014162	AR014162 Sequence
	c 45	14	0.8	33	6	AX067826	AX067826 Sequence

ALIGNMENTS

RESULT 1
AR032477
LOCUS AR032477 46 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 89 from patent US 5869241.
ACCESSION AR032477
VERSION AR032477.1 GI:5948082
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding molecule
JOURNAL Patent: US 5869241-A 89 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..46
/organism="unknown"
BASE COUNT 9 a 11 c 19 g 7 t
ORIGIN

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  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   2
I29217
LOCUS       I29217          46 bp    DNA             PAT       06-FEB-1997
DEFINITION  Sequence 89 from patent US 5578444.
ACCESSION   I29217
VERSION     I29217.1  GI:1820008
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence-directed DNA-binding molecules compositions and methods
  JOURNAL   Patent: US 5578444-A 89 26-NOV-1996;
FEATURES             Location/Qualifiers
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BASE COUNT        9 a      11 c      19 g       7 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 6.3e-14;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
           ||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   3
I90891
LOCUS       I90891          46 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 89 from patent US 5726014.
ACCESSION   I90891
VERSION     I90891.1  GI:3935361
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
  TITLE     Screening assay for the detection of DNA-binding molecules
  JOURNAL   Patent: US 5726014-A 89 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .46
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BASE COUNT        9 a      11 c      19 g       7 t
ORIGIN


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  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
           ||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   4
AX020418/c
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LOCUS       AX020418        24 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9935286.
ACCESSION   AX020418
VERSION     AX020418.1  GI:10044134
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kastelein,J.J. and Kuivenhoven,J.A.
  TITLE     Assay for predicting the angiographic response to lipid-lowering
            therapy in patients
  JOURNAL   Patent: WO 9935286-A 3 15-JUL-1999;
            KASTELEIN JOHANNES JACOBUS PIE (CA); AZ UNIV AMSTERDAM (NL);
            KUIVENHOVEN JAN ALBERT (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        6 a      8 c      3 g      7 t
ORIGIN


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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     343 agtcaagtatgggttgcacaa 363
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Db      24 AGTCAAGTATGGGTTGCACAA 4


RESULT   5
AR042917
LOCUS       AR042917        20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 3 from patent US 5814308.
ACCESSION   AR042917
VERSION     AR042917.1  GI:5963925
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,K.
  TITLE     Methods for the treatment of gastrointestinal tract disorders
  JOURNAL   Patent: US 5814308-A 3 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      4 c      5 g      5 t
ORIGIN


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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||
Db       2 TCCTGAAGGGACAGAT 17


RESULT   6
AR073289
LOCUS       AR073289        20 bp    DNA             PAT       28-AUG-2000
DEFINITION  Sequence 3 from patent US 5948892.
ACCESSION   AR073289
VERSION     AR073289.1  GI:10000052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wahl,R.C.
  TITLE     Analogs of macrophage stimulating protein
  JOURNAL   Patent: US 5948892-A 3 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      4 c      5 g      5 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 6.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    714 tcctgaagggacagat 729
          ||||||||||||||||
Db      2 TCCTGAAGGGACAGAT 17


RESULT   7
AX112428
LOCUS       AX112428       36 bp    DNA             PAT       01-MAY-2001
DEFINITION  Sequence 76 from Patent WO0127857.
ACCESSION   AX112428
VERSION     AX112428.1  GI:13939187
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Braun,A., Koester,H., van den Boom,D., Ping,Y., Rodi,C., He,L.,
            Chiu,N. and Jurinke,C.
  TITLE     Methods for generating databases and databases for identifying
            polymorphic genetic markers
  JOURNAL   Patent: WO 0127857-A 76 19-APR-2001;
            Sequenom, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .36
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                     /db_xref="taxon:32630"
                     /note="oligonucleotide primer"
BASE COUNT        8 a     10 c     11 g      7 t
ORIGIN


  Query Match             0.9%;  Score 16;  DB 6;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1377 agagcagctccgagtc 1392
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Db     21 AGAGCAGCTCCGAGTC 36


RESULT   8
DOG2155P01
LOCUS       DOG2155P01     22 bp    DNA             MAM       29-NOV-1996
DEFINITION  Canis familiaris (clone 2155F) DNA, STS primer.
ACCESSION   L78641
VERSION     L78641.1  GI:1372930
KEYWORDS    genetic marker; microsatellite; tetranucleotide repeat.
SOURCE      dog.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Francisco,L.V., Langston,A.A., Mellersh,C.S., Neal,C.L. and
            Ostrander,E.A.
  TITLE     A class of highly polymorphic tetranucleotide repeats for canine
            genetic mapping
  JOURNAL   Mamm. Genome 7 (5), 359-362 (1996)
  MEDLINE   96269603
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
                     /clone="2155F"
     primer_bind     complement(1. .22)
                     /note="2155F"
                     /evidence=experimental
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ORIGIN


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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||||
Db      8 GATGGAGACATTGGG 22


RESULT   9
AR130748/c
LOCUS       AR130748       22 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 4 from patent US 6190868.
ACCESSION   AR130748
VERSION     AR130748.1  GI:14119073
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Rothberg,J.M., Deem,M.W. and Simpson,J.W.
  TITLE     Method for identifying a nucleic acid sequence
  JOURNAL   Patent: US 6190868-A 4 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a      4 c      6 g      6 t
ORIGIN


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Qy   1436 cctgaggtcatgtct 1450
          |||||||||||||||
Db     18 CCTGAGGTCATGTCT 4


RESULT  10
E04451
LOCUS       E04451         25 bp    DNA             PAT       29-SEP-1997
DEFINITION  DNA encoding primer for detection of mutation at ornithine
            transcarbamylase(OTC) gene.
ACCESSION   E04451
VERSION     E04451.1  GI:2172652
KEYWORDS    JP 1993068600-A/11.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Matsuda,I., Shimada,K. and Matsuura,T.
  TITLE     OLIGONUCLEOTIDE AND DETECTION OF ORNITHINE TRANSCARBAMYLASE-MUTATED
            GENE WITH THE SAME
  JOURNAL   Patent: JP 1993068600-A 11 23-MAR-1993;
            MATSUDA ICHIRO, SHIMADA KAZUNORI, MATSUURA TOSHINOBU
COMMENT     OS   Artificial gene.
            OC   Artificial sequence; Genes.
            PN   JP 1993068600-A/11
            PD   23-MAR-1993
            PF   24-MAY-1991 JP 1991149718
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            PI   MATSUDA ICHIRO, SHIMADA KAZUNORI, MATSUURA TOSHINOBU PC
            C12Q1/68,A61B10/00,A61B10/00,C07H21/04,C12N15/10, PC
            C12N15/54//C12N9/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;.
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                      /db_xref="taxon:32630"
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ORIGIN


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Qy    687 atttcatctccttca 701
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Db      4 ATTTCATCTCCTTCA 18


RESULT  11
AR109648
LOCUS       AR109648        27 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 72 from patent US 6114139.
ACCESSION   AR109648
VERSION     AR109648.1  GI:12825924
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
  TITLE     G-protein coupled receptor protein and a DNA encoding the receptor
  JOURNAL   Patent: US 6114139-A 72 05-SEP-2000;
FEATURES              Location/Qualifiers
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ORIGIN


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Db      9 TGCTGGGCAATGCCC 23


RESULT  12
AX112429/c
LOCUS       AX112429        32 bp    DNA             PAT       01-MAY-2001
DEFINITION  Sequence 77 from Patent WO0127857.
ACCESSION   AX112429
VERSION     AX112429.1  GI:13939188
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Braun,A., Koester,H., van den Boom,D., Ping,Y., Rodi,C., He,L.,
            Chiu,N. and Jurinke,C.
  TITLE     Methods for generating databases and databases for identifying
            polymorphic genetic markers
  JOURNAL   Patent: WO 0127857-A 77 19-APR-2001;
            Sequenom, Inc. (US)
FEATURES              Location/Qualifiers
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Qy   1396 ccagagcttcctgca 1410
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Db     32 CCAGAGCTTCCTGCA 18


RESULT  13
A48824
LOCUS       A48824          41 bp    DNA             PAT       07-MAR-1997
DEFINITION  Sequence 16 from Patent EP0704527.
ACCESSION   A48824
VERSION     A48824.1  GI:2302486
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Mestric,S., Punt,P.J., Valinger,R., Van and Den,H.C.
  TITLE     DNA sequences encoding biosynthetic insulin precursors and process
            for prepation of insulin
  JOURNAL   Patent: EP 0704527-A 16 03-APR-1996;
            PLIVA PHARM & CHEM WORKS (YU)
COMMENT     Other publication CN 1126761 960717
            Other publication CA 2155451 960206
            Other publication SK 97195 960207
            Other publication SI 9500250 960229
            Other publication BG 99844 960229
            Other publication CZ 9501999 960214
            Other publication PL 309882 960219.
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     source           1. .41
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                      /db_xref="taxon:32644"
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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    396 gccaggtggagctgg 410
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Db     17 GCCAGGTGGAGCTGG 31


RESULT  14
AX167117/c
LOCUS       AX167117        20 bp    DNA             PAT       03-JUL-2001
DEFINITION  Sequence 4 from Patent WO0144455.
ACCESSION   AX167117
VERSION     AX167117.1  GI:14596605
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Beri,R.
  TITLE     Antisense oligonucleotides
  JOURNAL   Patent: WO 0144455-A 4 21-JUN-2001;
            AstraZeneca AB (SE)
FEATURES              Location/Qualifiers
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RESULT  15
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LOCUS       AR069484       21 bp    DNA             PAT       18-FEB-2000
DEFINITION  Sequence 21 from patent US 5891666.
ACCESSION   AR069484
VERSION     AR069484.1  GI:7220372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matsuyama,T. and Grossman,A.
  TITLE     Genes encoding LSIRF polypeptides
  JOURNAL   Patent: US 5891666-A 21 06-APR-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        3 a      9 c      5 g      4 t
ORIGIN


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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||
Db      7 CAGCTCCGAGTCCA 20


RESULT  16
AX146446
LOCUS       AX146446       22 bp    DNA             PAT       31-MAY-2001
DEFINITION  Sequence 27 from Patent WO0134647.
ACCESSION   AX146446
VERSION     AX146446.1  GI:14284864
KEYWORDS    .
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Bell,M.P., Neff,T.B., Polarek,J.W. and Seeley,T.W.
  TITLE     Animal collagens and gelatins
  JOURNAL   Patent: WO 0134647-A 27 17-MAY-2001;
            FIBROGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
BASE COUNT        3 a     10 c      5 g      4 t
ORIGIN


  Query Match              0.8%;  Score 14;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    154 cctggccctgctgg 167
          ||||||||||||||
Db      2 CCTGGCCCTGCTGG 15


RESULT  17
AX146447/c
LOCUS       AX146447       22 bp    DNA             PAT       31-MAY-2001
DEFINITION  Sequence 28 from Patent WO0134647.
ACCESSION   AX146447
VERSION     AX146447.1  GI:14284865
KEYWORDS    .
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Bell,M.P., Neff,T.B., Polarek,J.W. and Seeley,T.W.
  TITLE     Animal collagens and gelatins
  JOURNAL   Patent: WO 0134647-A 28 17-MAY-2001;
            FIBROGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
BASE COUNT        4 a      5 c     10 g      3 t
ORIGIN


  Query Match              0.8%;  Score 14;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    154 cctggccctgctgg 167
          ||||||||||||||
Db     21 CCTGGCCCTGCTGG 8


RESULT  18
A84872/c
LOCUS       A84872         23 bp    DNA             PAT       21-JAN-2000
DEFINITION  Sequence 21 from Patent WO9844106.
ACCESSION   A84872
VERSION     A84872.1  GI:6733720
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Waeber,G. and Bonny,C.
  TITLE     TRANSCRIPTION FACTOR ISLET-BRAIN 1 (IB1)
  JOURNAL   Patent: WO 9844106-A 21 08-OCT-1998;
            WAEBER GERARD (CH); NICOD PASCAL (CH)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      8 c      4 g      6 t
ORIGIN


  Query Match              0.8%;  Score 14;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1548 tgctgcagatggac 1561
          ||||||||||||||
Db     19 TGCTGCAGATGGAC 6
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RESULT  19
AX077382/c
LOCUS       AX077382       23 bp    DNA             PAT       22-FEB-2001
DEFINITION  Sequence 34 from Patent WO0105952.
ACCESSION   AX077382
VERSION     AX077382.1  GI:13121937
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   van der Biezen,E.A. and Jones,J.D.
  TITLE     Rela/spot homologues from plant
  JOURNAL   Patent: WO 0105952-A 34 25-JAN-2001;
            Plant Bioscience Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        5 a      6 c      8 g      4 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    855 cctcctacctggag 868
          ||||||||||||||
Db     14 CCTCCTACCTGGAG 1


RESULT  20
AX148006/c
LOCUS       AX148006       23 bp    DNA             PAT       08-JUN-2001
DEFINITION  Sequence 6 from Patent WO0134848.
ACCESSION   AX148006
VERSION     AX148006.1  GI:14346977
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Brown,B.A., Kilpatrick,D.R., Pallansch,M.A. and Oberste,M.S.
  TITLE     Serotype-specific identification of enterovirus 71 by rt-pcr
  JOURNAL   Patent: WO 0134848-A 6 17-MAY-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      3 c     10 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    227 accaagcctgccct 240
          ||||||||||||||
Db     20 ACCAAGCCTGCCCT 7


RESULT  21
AR130317/c
LOCUS       AR130317       25 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 27 from patent US 6187913.
ACCESSION   AR130317
VERSION     AR130317.1  GI:14118214
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Blumenfeld,M. and Merenkova,I.
  TITLE     Covalently crosslinked oligonucleotides, preparation method and
            synthon which is of use in the method
  JOURNAL   Patent: US 6187913-A 27 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        6 a      7 c      7 g      5 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1527 tcactcgagatggc 1540
          ||||||||||||||
Db     14 TCACTCGAGATGGC 1


RESULT  22
AR130321/c
LOCUS       AR130321       25 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 31 from patent US 6187913.
ACCESSION   AR130321
VERSION     AR130321.1  GI:14118218
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Blumenfeld,M. and Merenkova,I.
  TITLE     Covalently crosslinked oligonucleotides, preparation method and
            synthon which is of use in the method
  JOURNAL   Patent: US 6187913-A 31 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        6 a      7 c      7 g      5 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1527 tcactcgagatggc 1540
          ||||||||||||||
Db     14 TCACTCGAGATGGC 1


RESULT  23
AR090227/c
LOCUS       AR090227       26 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 347 from patent US 5994076.
ACCESSION   AR090227
VERSION     AR090227.1  GI:10016982
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 347 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        5 a      9 c      7 g      5 t
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ORIGIN

  Query Match             0.8%;  Score 14;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1105 ccaagaggttgtcg 1118
          ||||||||||||||
Db     24 CCAAGAGGTTGTCG 11


RESULT  24
AR091212
LOCUS       AR091212       26 bp    DNA              PAT       07-SEP-2000
DEFINITION  Sequence 1332 from patent US 5994076.
ACCESSION   AR091212
VERSION     AR091212.1  GI:10017967
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 1332 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        4 a      9 c      6 g      7 t
ORIGIN

  Query Match             0.8%;  Score 14;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     77 tacgggctccaggc 90
          ||||||||||||||
Db      4 TACGGGCTCCAGGC 17


RESULT  25
AX037841/c
LOCUS       AX037841       26 bp    DNA              PAT       16-NOV-2000
DEFINITION  Sequence 192 from Patent WO0059917.
ACCESSION   AX037841
VERSION     AX037841.1  GI:11227223
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Howard,J.C., Feldkamp,U., Rauhe,H. and Banzhaf,W.
  TITLE     Information-carrying and information-processing polymers
  JOURNAL   Patent: WO 0059917-A 192 12-OCT-2000;
            HOWARD JONATHAN C (DE) ; FELDKAMP UDO (DE) ; RAUHE HILMAR (DE) ;
            BANZHAF WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="X83L: Unique non-biological sequence for
                     representation of data."
BASE COUNT        4 a      5 c      9 g      8 t
ORIGIN

  Query Match             0.8%;  Score 14;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1156 cctcaagatgccca 1169
          ||||||||||||||
Db     16 CCTCAAGATGCCCA 3


RESULT  26
A91913
LOCUS       A91913         27 bp    DNA              PAT       22-JAN-2000
DEFINITION  Sequence 1 from Patent WO9822606.
ACCESSION   A91913
VERSION     A91913.1  GI:6740780
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Rouy,D. and Benoit,P.
  TITLE     RECOMBINANT BICISTRON ADENOVIRUS FOR TREATING PATHOLOGICAL
            CONDITIONS LINKED WITH DYSLIPOPROTEINEMIA
  JOURNAL   Patent: WO 9822606-A 1 28-MAY-1998;
            ROUY DIDIER (FR); BENOIT PATRICK (FR)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        6 a      8 c      8 g      5 t
ORIGIN

  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    120 gcctgataaccatg 133
          ||||||||||||||
Db      1 GCCTGATAACCATG 14


RESULT  27
AR026695
LOCUS       AR026695       27 bp    DNA              PAT       29-SEP-1999
DEFINITION  Sequence 16 from patent US 5856134.
ACCESSION   AR026695
VERSION     AR026695.1  GI:5937535
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5856134-A 16 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN

  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
          ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  28
AR026699/c
LOCUS       AR026699       27 bp    DNA              PAT       29-SEP-1999
DEFINITION  Sequence 21 from patent US 5856134.
ACCESSION   AR026699
VERSION     AR026699.1  GI:5937539
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5856134-A 21 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      7 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db     21 ACTGAGAGCAGCTC 8


RESULT  29
AR026713
LOCUS       AR026713       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 35 from patent US 5856134.
ACCESSION   AR026713
VERSION     AR026713.1  GI:5937553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5856134-A 35 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  30
AR026714
LOCUS       AR026714       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 36 from patent US 5856134.
ACCESSION   AR026714
VERSION     AR026714.1  GI:5937554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5856134-A 36 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  31
AR029305
LOCUS       AR029305       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 27 from patent US 5859230.
ACCESSION   AR029305
VERSION     AR029305.1  GI:5941278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Reyes,G.R. and Young,L.Marie.
  TITLE     Non-A/non-B/non-C/non-D/non-E hepatitis agents and molecular
            cloning thereof
  JOURNAL   Patent: US 5859230-A 27 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  32
AR049121
LOCUS       AR049121       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 16 from patent US 5824507.
ACCESSION   AR049121
VERSION     AR049121.1  GI:6005160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5824507-A 16 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  33
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AR049125/c
LOCUS       AR049125       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 21 from patent US 5824507.
ACCESSION   AR049125
VERSION     AR049125.1  GI:6005164
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5824507-A 21 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      7 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db     21 ACTGAGAGCAGCTC 8


RESULT  34
AR049139
LOCUS       AR049139       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 35 from patent US 5824507.
ACCESSION   AR049139
VERSION     AR049139.1  GI:6005178
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5824507-A 35 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  35
AR049140
LOCUS       AR049140       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 36 from patent US 5824507.
ACCESSION   AR049140
VERSION     AR049140.1  GI:6005179
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5824507-A 36 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  36
AR065379
LOCUS       AR065379       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 16 from patent US 5849532.
ACCESSION   AR065379
VERSION     AR065379.1  GI:5995595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5849532-A 16 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  37
AR065383/c
LOCUS       AR065383       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 21 from patent US 5849532.
ACCESSION   AR065383
VERSION     AR065383.1  GI:5995599
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5849532-A 21 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      7 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
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Db      21 ACTGAGAGCAGCTC 8


RESULT  38
AR065397
LOCUS       AR065397       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 35 from patent US 5849532.
ACCESSION   AR065397
VERSION     AR065397.1  GI:5995613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5849532-A 35 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  39
AR065398
LOCUS       AR065398       27 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 36 from patent US 5849532.
ACCESSION   AR065398
VERSION     AR065398.1  GI:5995614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
  TITLE     Hepatitis G virus and molecular cloning thereof
  JOURNAL   Patent: US 5849532-A 36 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      5 c      9 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1373 actgagagcagctc 1386
           ||||||||||||||
Db      7 ACTGAGAGCAGCTC 20


RESULT  40
I22030/c
LOCUS       I22030         28 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 4 from patent US 5525504.
ACCESSION   I22030
VERSION     I22030.1  GI:1602384
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Goebel,W., Libby,S.J. and Heffron,F.
  TITLE     Cytolysin gene and gene product
  JOURNAL   Patent: US 5525504-A 4 11-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT       11 a      3 c      7 g      7 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    686 aatttcatctcctt 699
          ||||||||||||||
Db     19 AATTTCATCTCCTT 6


RESULT  41
AX167972/c
LOCUS       AX167972       31 bp    DNA             PAT       03-JUL-2001
DEFINITION  Sequence 156 from Patent WO0142307.
ACCESSION   AX167972
VERSION     AX167972.1  GI:14597292
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 156 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide primer for mutagenesis"
BASE COUNT        5 a      9 c     10 g      7 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    144 cagtcctgaccctg 157
          ||||||||||||||
Db     19 CAGTCCTGACCCTG 6


RESULT  42
AX107235
LOCUS       AX107235       32 bp    DNA             PAT       30-APR-2001
DEFINITION  Sequence 54 from Patent WO0123606.
ACCESSION   AX107235
VERSION     AX107235.1  GI:13922720
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Grabowski,R. and Berghof,K.
  TITLE     Nucleic acid molecules for detecting bacteria and phylogenetic
            units of bacteria
  JOURNAL   Patent: WO 0123606-A 54 05-APR-2001;
            Biotecon Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
```

```
                     /note="abgeleitetet von Gattungen der Enterobakterien"
BASE COUNT        9 a      6 c     12 g      5 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    712 ggtcctgaagggac 725
          ||||||||||||||
Db      3 GGTCCTGAAGGGAC 16


RESULT  43
AX107358
LOCUS       AX107358       32 bp    DNA             PAT       30-APR-2001
DEFINITION  Sequence 177 from Patent WO0123606.
ACCESSION   AX107358
VERSION     AX107358.1  GI:13922843
KEYWORDS    .
SOURCE      Pantoea dispersa.
  ORGANISM  Pantoea dispersa
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Pantoea.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Grabowski,R. and Berghof,K.
  TITLE     Nucleic acid molecules for detecting bacteria and phylogenetic
            units of bacteria
  JOURNAL   Patent: WO 0123606-A 177 05-APR-2001;
            Biotecon Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Pantoea dispersa"
                     /db_xref="taxon:59814"
BASE COUNT        9 a      7 c     13 g      3 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    712 ggtcctgaagggac 725
          ||||||||||||||
Db      3 GGTCCTGAAGGGAC 16


RESULT  44
AR014162/c
LOCUS       AR014162       33 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 4 from patent US 5773252.
ACCESSION   AR014162
VERSION     AR014162.1  GI:3971616
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Greene,J.M. and Rosen,C.A.
  TITLE     Fibroblast growth factor 15
  JOURNAL   Patent: US 5773252-A 4 30-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        5 a      6 c      9 g     13 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1168 caagatctcctgcc 1181
          ||||||||||||||
Db     14 CAAGATCTCCTGCC 1


RESULT  45
AX067826/c
LOCUS       AX067826       33 bp    DNA             PAT       19-JAN-2001
DEFINITION  Sequence 63 from Patent WO0077043.
ACCESSION   AX067826
VERSION     AX067826.1  GI:12329704
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.
  TITLE     Dna vaccines for pets and sport animals
  JOURNAL   Patent: WO 0077043-A 63 21-DEC-2000;
            MERIAL (FR)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucl otide"
BASE COUNT        9 a      6 c      9 g      9 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1750 ctatcctaaaggcc 1763
          ||||||||||||||
Db     20 CTATCCTAAAGGCC 7


Search completed: April 20, 2002, 01:08:26
Job time: 11465 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2002, 23:59:08 ; Search time 184.86 Seconds
(without alignments)
8287.570 Million cell updates/sec

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Perfect score: 1787
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 989696

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	2.6	46	15	AAQ69339	Human CETP gene, t
2	46	2.6	46	18	AAT63801	Human cholesteryl
3	46	2.6	46	20	AAX17089	Test sequence from
4	34	1.9	34	20	AAX36594	PCR primer for Mam
c 5	30	1.7	30	20	AAX22540	Human CETP DNA fra
c 6	27	1.5	40	20	AAX36595	PCR primer for Mam
c 7	21	1.2	24	20	AAX86985	Cholesteryl ester
8	18	1.0	18	17	AAT50642	Human CETP hairpin
9	18	1.0	18	17	AAT50596	Human CETP hairpin
10	18	1.0	18	17	AAT50597	Human CETP hairpin
11	18	1.0	18	17	AAT50598	Human CETP hairpin
12	18	1.0	18	17	AAT50599	Human CETP hairpin
13	18	1.0	18	17	AAT50600	Human CETP hairpin
14	18	1.0	18	17	AAT50601	Human CETP hairpin
15	18	1.0	18	17	AAT50602	Human CETP hairpin
16	18	1.0	18	17	AAT50603	Human CETP hairpin
17	18	1.0	18	17	AAT50604	Human CETP hairpin
18	18	1.0	18	17	AAT50605	Human CETP hairpin
19	18	1.0	18	17	AAT50606	Human CETP hairpin
20	18	1.0	18	17	AAT50607	Human CETP hairpin
21	18	1.0	18	17	AAT50608	Human CETP hairpin
22	18	1.0	18	17	AAT50609	Human CETP hairpin
23	18	1.0	18	17	AAT50610	Human CETP hairpin
24	18	1.0	18	17	AAT50611	Human CETP hairpin
25	18	1.0	18	17	AAT50612	Human CETP hairpin
26	18	1.0	18	17	AAT50613	Human CETP hairpin
27	18	1.0	18	17	AAT50614	Human CETP hairpin
28	18	1.0	18	17	AAT50615	Human CETP hairpin
29	18	1.0	18	17	AAT50616	Human CETP hairpin
30	18	1.0	18	17	AAT50617	Human CETP hairpin
31	18	1.0	18	17	AAT50618	Human CETP hairpin
32	18	1.0	18	17	AAT50619	Human CETP hairpin
33	18	1.0	18	17	AAT50620	Human CETP hairpin
34	18	1.0	18	17	AAT50621	Human CETP hairpin
35	18	1.0	18	17	AAT50622	Human CETP hairpin
36	18	1.0	18	17	AAT50623	Human CETP hairpin
37	18	1.0	18	17	AAT50624	Human CETP hairpin
38	18	1.0	18	17	AAT50625	Human CETP hairpin
39	18	1.0	18	17	AAT50743	Rabbit CETP hairpi
40	18	1.0	18	17	AAT50626	Human CETP hairpin
41	18	1.0	18	17	AAT50627	Human CETP hairpin
42	18	1.0	18	17	AAT50628	Human CETP hairpin
43	18	1.0	18	17	AAT50629	Human CETP hairpin
44	18	1.0	18	17	AAT50630	Human CETP hairpin
45	18	1.0	18	17	AAT50631	Human CETP hairpin

ALIGNMENTS

RESULT 1
AAQ69339
ID AAQ69339 standard; DNA; 46 BP.
XX
AC AAQ69339;
XX
DT 22-FEB-1995 (first entry)
XX
DE Human CETP gene, target region.
XX
KW DNA protein-binding assay; test sequence; screening sequence;
KW promoter; target; TATA box; Herpes Simplex Virus; HSV;
KW origin of replication; UL9; transcription factor; TFIID;
KW CETP; cholesteryl ester transferase protein; ds.
XX
OS Synthetic.
XX
PN WO9414980-A.
XX
PD 07-JUL-1994.
XX
PF 20-DEC-1993; 93WO-US12388.
XX
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1994-234711/28.
XX
PT Sequence-directed DNA-binding molecules - useful in
PT pharmaceuticals and as molecular reagents

```
XX
PS   Claim 28; Page 256; 587pp; English.
XX
CC   A DNA protein-binding assay is provided, useful for screening
CC   libraries of synthetic or biological cpds. for their ability
CC   to bind DNA test sequences.  The assay is versatile in that any
CC   number of test sequences can be tested by placing the test sequence
CC   adjacent to a defined protein-binding screening sequence.  Binding
CC   of mols. to these test sequences changes the binding characteristics
CC   of the protein mol. to its cognate binding sequence.  When such a mol.
CC   binds the test sequence, the equilibrium of the DNA:protein complexes
CC   is disturbed, generating changes in the concentration of free DNA probe.
CC   One application of this method is to eucaryotic general transcription
CC   factors (e.g. TFIID), where the target region is typically selected
CC   from DNA sequences adjacent to the binding site for the eucaryotic
CC   transcription factor.  Numerous exemplary test sequences are given:
CC   the sequences in AAQ69251-731 and AAQ69850 correspond to promoter
CC   targets (typically, TATA box-contg. sites) for human genes and the
CC   sequences in AAQ69732-849 correspond to promoter targets for viral genes.
CC    The test sequences may also be randomly generated.  DNA:protein
CC   interaction may be used for screening purposes, e.g. the Herpes Simplex
CC   Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and
CC   AAQ69891).
XX
SQ   Sequence 46 BP; 9 A; 11 C; 19 G; 7 T; 0 other;


  Query Match             2.6%;  Score 46;  DB 15;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-12;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
           |||||||||||||||||||||||||||||||||||||||||||||
Db       1 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 46


RESULT   2
AAT63801
ID   AAT63801 standard; DNA; 46 BP.
XX
AC   AAT63801;
XX
DT   13-MAR-1997  (first entry)
XX
DE   Human cholesteryl ester transferase protein gene TFIID binding site.
XX
KW   Duplex DNA; target region; binding characteristic; DNA binding protein;
KW   TFIID; transcription factor; binding site; inhibition; enhance; CETP;
KW   cancer; inherited genetic disorder; ds.
XX
OS   Homo sapiens.
XX
PN   US5578444-A.
XX
PD   26-NOV-1996.
XX
PF   27-JUN-1991;   91US-0723618.
XX
PR   20-DEC-1993;   93US-0171389.
PR   27-JUN-1991;   91US-0723618.
PR   23-DEC-1992;   92US-0996783.
PR   17-SEP-1993;   93US-0123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Andrews BM,  Cantor CR,  Edwards CA,  Fry KE,  Turin LM;
XX
DR   WPI; 1997-020402/02.
XX
PT   Altering binding characteristics of DNA binding proteins to duplex
PT   DNA - by attaching specific small cpd. to target region close to the
PT   protein's binding site, useful in treatment of viral disease, cancer
PT   etc
XX
PS   Claim 6; Column 143; 264pp; English.
XX
CC   The sequences given in AAT63713-4312 represent duplex DNA's which act
CC   as target regions in the method of the invention.  The method for
CC   altering the binding characteristics of a DNA-binding protein to duplex
CC   DNA comprises contacting the duplex DNA with a small molecule which
CC   binds sequence-specifically to a target region, where, when the small
CC   molecule is bound to the target region, it is adjacent to, but not
CC   overlapping by more than 4 bp, a binding site for a DNA-binding protein.
CC   The small molecule is added at a concentration effective to alter the
CC   binding of the DNA binding protein, pref. TFIID, to its binding site on
CC   the duplex DNA.  The binding of the small molecule may inhibit or
CC   enhance the binding of the DNA-binding protein to its binding site.  The
CC   compounds isolated using this method are potentially useful as
CC   therapeutic agents for treatment of any disease which involves a
CC   specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
CC   The method is suitable for screening large biological or chemical
CC   libraries and allows determination of sequence-specific and relative
CC   affinities of known DNA-binding agents for different DNA sequences.
CC   The design of these duplex DNA's allows a single DNA:protein interaction
CC   to be used for screening sequence-specific, or preferential, DNA binding
CC   proteins that recognise almost any possible sequence (see also AAT49539-
CC   74).
XX
SQ   Sequence 46 BP; 9 A; 11 C; 19 G; 7 T; 0 other;


  Query Match             2.6%;  Score 46;  DB 18;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-12;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
           |||||||||||||||||||||||||||||||||||||||||||||
Db       1 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 46


RESULT   3
AAX17089
ID   AAX17089 standard; DNA; 46 BP.
XX
AC   AAX17089;
XX
DT   06-MAY-1999  (first entry)
XX
DE   Test sequence from human cholesteryl ester transferase protein gene.
XX
KW   Test sequence; DNA-binding molecule; screening sequence; human;
KW   nucleic acid amplification; target; viral; ds.
XX
OS   Homo sapiens.
XX
PN   US5869241-A.
XX
PD   09-FEB-1999.
XX
PF   07-JUN-1995;   95US-0475228.
XX
PR   20-DEC-1993;   93US-0171389.
PR   27-JUN-1991;   91US-0723618.
PR   23-DEC-1992;   92US-0996783.
PR   17-SEP-1993;   93US-0123936.
PR   07-JUN-1995;   95US-0475228.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Andrews BM,  Cantor CR,  Edwards CA,  Fry KE,  Turin LM;
XX
DR   WPI; 1999-152755/13.
XX
PT   Determination of DNA sequence preference of a DNA-binding molecule -
PT   based on inhibition of binding of protein to oligonucleotide
PT   sequence attached to test sequence
```

```
XX
PS   Claim 3; Columns 145-146; 270pp; English.
XX
CC   Sequences AAX17001 to AAX17600 represent specifically claimed target
CC   test sequences that are used in the method of the invention of
CC   determining the DNA sequence preference of a DNA-binding molecule. The
CC   method comprises: (i) adding a test molecule and a DNA-binding protein to
CC   a mixture of duplex DNA test oligonucleotides, each of the test
CC   oligonucleotides having a test sequence adjacent to a screening sequence,
CC   where the screening sequence binds to the DNA-binding protein with a
CC   binding affinity that is independent of the DNA sequence of the test
CC   sequence, and where the mixture of duplex DNA test oligonucleotides
CC   includes several test sequences; (ii) incubating the test molecule, the
CC   mixture of duplex DNA test oligonucleotides and the DNA-binding protein
CC   for a time sufficient to permit binding of the test molecule to test
CC   sequences in the duplex DNA; (iii) separating unbound test
CC   oligonucleotides from test oligonucleotides bound to binding protein;
CC   (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
CC   (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
CC   (vii) sequencing the isolated test oligonucleotides. Test sequences
CC   AAX17001-X17481 and AAX17600 correspond to promoter targets for human
CC   genes and test sequences AAX17482-X17599 correspond to promoter targets
CC   for viral genes.
XX
SQ   Sequence 46 BP; 9 A; 11 C; 19 G; 7 T; 0 other;


  Query Match             2.6%;  Score 46;  DB 20;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-12;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
           ||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 46


RESULT - 4
AAX36594
ID   AAX36594 standard; DNA; 34 BP.
XX
AC   AAX36594;
XX
DT   08-JUL-1999  (first entry)
XX
DE   PCR primer for Mammalian CETP immunogenic fragment coding sequence.
XX
KW   CETP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW   antibody production; cholesteryl ester transfer; therapy;
KW   high density lipoprotein; HDL cholesterol concentration;
KW   pro-atherogenic dyslipoproteinaemia; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9915655-A1.
XX
PD   01-APR-1999.
XX
PF   17-SEP-1998;   98WO-US19366.
XX
PR   19-SEP-1997;   97US-0934367.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Glenn K,  Needleman P;
XX
DR   WPI; 1999-276984/23.
XX
PT   New recombinant DNA vaccines
XX
PS   Example 3; Page 49; 99pp; English.
XX
CC   This sequence is a PCR primer for DNA encoding an immunogenic fragment of
CC   the human cholesteryl ester transferase protein (CETP).
CC   The invention relates to recombinant DNA vaccines that contain DNA
CC   encoding CETP, which can be used for producing antibodies to lessen the
CC   transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC   method can provide an autogenic immunological process for lessening the
CC   transfer of cholesteryl esters from HDL particles and for increasing the
CC   HDL cholesterol concentration of a mammal whose blood also contains
CC   CETP. The method may be useful in treating human pro-atherogenic
CC   dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC   method can have an effect that lasts for months as compared to the
CC   short-term effects of the small molecule drugs now available.
XX
SQ   Sequence 34 BP; 6 A; 9 C; 9 G; 10 T; 0 other;


  Query Match             1.9%;  Score 34;  DB 20;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1522 gattatcactcgagatggcttcctgctgctgcag 1555
           ||||||||||||||||||||||||||||||||||
Db       1 gattatcactcgagatggcttcctgctgctgcag 34


RESULT   5
AAX22540/c
ID   AAX22540 standard; DNA; 30 BP.
XX
AC   AAX22540;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human CETP DNA fragment #1.
XX
KW   CETP; cholesteryl ester transfer protein; inhibitor; therapy; treatment;
KW   surface plasmon resonance; vascular disease; pathogenic; atherosclerosis;
KW   human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19731609-A1.
XX
PD   18-FEB-1999.
XX
PF   23-JUL-1997;   97DE-1031609.
XX
PR   23-JUL-1997;   97DE-1031609.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI   Budzinksi R,  Krist B,  Mark M,  Mueller P;
XX
DR   WPI; 1999-143775/13.
XX
PT   RNA transcript of human cholesteryl ester transfer protein gene -
PT   useful in drug screening assays, especially for atherosclerosis
XX
PS   Claim 31; Page 9; 24pp; German.
XX
CC   This invention describes the isolation of a transcript of the human
CC   cholesteryl ester transfer protein (CETP) gene having a 5' untranslated
CC   region including a regulatory sequence. The invention also describes
CC   a method (a) for identifying substances capable of inhibiting CETP gene
CC   expression, comprising measuring the translation rate of the above
CC   transcript in the presence of a test substance, (2) a test substance
CC   capable of inhibiting CETP gene expression, (3) an antisense
CC   oligonucleotide capable of binding to the 5' untranslated region of the
CC   above transcript and (4) a method based on surface plasmon resonance for
CC   measuring the binding of a substance to a nucleic acid. The test
CC   substance of (2) and the oligonucleotide of (3) are useful for
CC   prophylactic or therapeutic treatment of vascular diseases in which CETP
CC   has a pathogenic role, especially atherosclerosis.
XX
```

```
SQ   Sequence 30 BP; 6 A; 3 C; 12 G; 9 T; 0 other;

  Query Match             1.7%;  Score 30;  DB 20;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    105 cacttacacaccactgcctgataaccatgc 134
          ||||||||||||||||||||||||||||||
Db     30 CACTTACACACCACTGCCTGATAACCATGC 1


RESULT   6
AAX36595/c
ID   AAX36595 standard; DNA; 40 BP.
XX
AC   AAX36595;
XX
DT   08-JUL-1999  (first entry)
XX
DE   PCR primer for Mammalian CETP immunogenic fragment coding sequence.
XX
KW   CETP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW   antibody production; cholesteryl ester transfer; therapy;
KW   high density lipoprotein; HDL cholesterol concentration;
KW   pro-atherogenic dyslipoproteinaemia; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9915655-A1.
XX
PD   01-APR-1999.
XX
PF   17-SEP-1998;   98WO-US19366.
XX
PR   19-SEP-1997;   97US-0934367.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Glenn K,  Needleman P;
XX
DR   WPI; 1999-276984/23.
XX
PT   New recombinant DNA vaccines
XX
PS   Example 3; Page 50; 99pp; English.
XX
CC   This sequence is a PCR primer for DNA encoding an immunogenic fragment of
CC   the human cholesteryl ester transferase protein (CETP).
CC   The invention relates to recombinant DNA vaccines that contain DNA
CC   encoding CETP, which can be used for producing antibodies to lessen the
CC   transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC   method can provide an autogenic immunological process for lessening the
CC   transfer of cholesteryl esters from HDL particles and for increasing the
CC   HDL cholesterol concentration of a mammal whose blood also contains
CC   CETP. The method may be useful in treating human pro-atherogenic
CC   dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC   method can have an effect that lasts for months as compared to the
CC   short-term effects of the small molecule drugs now available.
XX
SQ   Sequence 40 BP; 12 A; 11 C; 10 G; 7 T; 0 other;

  Query Match             1.5%;  Score 27;  DB 20;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.0038;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1583 ctggtggatttcctccagagcttgagc 1609
          ||||||||||||||||||||||||||
Db     40 CTGGTGGATTTCCTCCAGAGCTTGAGC 14


RESULT   7
AAX86985/c
ID   AAX86985 standard; DNA; 24 BP.
XX
AC   AAX86985;
XX
DT   24-SEP-1999  (first entry)
XX
DE   Cholesteryl ester transfer protein (CETP) gene amplifying reverse primer.
XX
KW   Lipid-lowering therapy; LLT; coronary artery disease; CAD; CETP;
KW   TaqIB restriction site; cholesterol ester transfer protein; HDL;
KW   high-density lipoprotein; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9935286-A2.
XX
PD   15-JUL-1999.
XX
PF   06-JAN-1999;   99WO-EP00150.
XX
PR   07-JAN-1998;   98EP-0200022.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Kastelein JJP,  Kuivenhoven JA;
XX
DR   WPI; 1999-444202/37.
XX
PT   Assay for testing the genetic predisposition to respond to
PT   lipid-lowering therapy in patients with coronary artery disease
PT   (CAD)
XX
PS   Claim 2; Page 20; 25pp; English.
XX
CC   The invention relates to an assay for testing the genetic predisposition
CC   to respond to lipid-lowering therapy (LLT) in patients with coronary
CC   artery disease (CAD). The method comprises detecting a TaqIB restriction
CC   site in intron 1 of both alleles of the cholesterol ester transfer
CC   protein (CETP) gene by a suitable technique, and correlating the
CC   presence of the site with a high or intermediate susceptibility for LLT.
CC   The TaqIB polymorphism in the CETP gene is associated with an effect on
CC   lipid transfer activity and high-density lipoprotein (HDL) levels. This
CC   facilitates predicting the success of LLT's in patients. Sequences
CC   AAX86984-85 represent PCR primers derived from the CETP gene and are
CC   used for testing the predisposition to respond to LLT in patients with
CC   CAD.
XX
SQ   Sequence 24 BP; 6 A; 8 C; 3 G; 7 T; 0 other;

  Query Match             1.2%;  Score 21;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    343 agtcaagtatgggttgcacaa 363
          |||||||||||||||||||||
Db     24 AGTCAAGTATGGGTTGCACAA 4


RESULT   8
AAT50642
ID   AAT50642 standard; RNA; 18 BP.
XX
AC   AAT50642;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #1669.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
```

```
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C;  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 54; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 91;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1663 gctcacagctggaaccct 1680
           ||:||||||:|||||||:
Db       1 gcucacagcuggaacccu 18


RESULT   9
AAT50596
ID   AAT50596 standard; RNA; 18 BP.
XX
AC   AAT50596;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #30.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 7 C; 6 G; 2 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 91;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     24 ccctgctgcccggaagag 41
          |||:||:||||||||||
Db      1 cccugcugcccggaagag 18


RESULT  10
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AAT50597
ID   AAT50597 standard; RNA; 18 BP.
XX
AC   AAT50597;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #96.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 7 C; 6 G; 2 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 91;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      90 ctgaacggctcgggccac 107
           |:|||||||:||||||||
Db       1 cugaacggcucgggccac 18


RESULT  11
AAT50598
ID   AAT50598 standard; RNA; 18 BP.
XX
AC   AAT50598;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #119.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 5 A; 8 C; 2 G; 3 U; 0 other;
```

```
  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 91;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     113 caccactgcctgataacc 130
           ||||||:|||:||:||||
Db       1 caccacugccugauaacc 18


RESULT  12
AAT50599
ID   AAT50599 standard; RNA; 18 BP.
XX
AC   AAT50599;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #145.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins. The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP. The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels. The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis. By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels). The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 3 G; 4 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     139 tgccacagtcctgaccct 156
           :|||||||:||:|||||:
Db       1 ugccacaguccugacccu 18


RESULT  13
AAT50600
ID   AAT50600 standard; RNA; 18 BP.
XX
AC   AAT50600;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #150.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins. The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP. The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels. The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis. By inhibiting CETP, the levels of HDL and low density
```

CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 2 A; 9 C; 4 G; 3 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 144 cagtcctgaccctggccc 161
||||:||:||||||:|||||
Db 1 caguccugacccuggccc 18

RESULT 14
AAT50601
ID AAT50601 standard; RNA; 18 BP.
XX
AC AAT50601;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #162.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 52; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 2 A; 5 C; 7 G; 4 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 156 tggccctgctgggcaatg 173
:|||||:||:|||||:|
Db 1 uggcccugcugggcaaug 18

RESULT 15
AAT50602
ID AAT50602 standard; RNA; 18 BP.
XX
AC AAT50602;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #182.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 52; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby

```
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 91;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    176 catgcctgctccaaaggc 193
          ||:|||:||:||||||||
Db      1 caugccugcuccaaaggc 18


RESULT  16
AAT50603
ID   AAT50603 standard; RNA; 18 BP.
XX
AC   AAT50603;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #235.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    229 caagcctgccctcctggt 246
          ||||||:||||:||:||:
Db      1 caagccugcccuccuggu 18


RESULT  17
AAT50604
ID   AAT50604 standard; RNA; 18 BP.
XX
AC   AAT50604;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #276.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
```

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XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 3 G; 4 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches  14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    270 tgatccagaccgccttcc 287
          :||:||||||||||::||
Db      1 ugauccagaccgccuucc 18


RESULT  18
AAT50605
ID   AAT50605 standard; RNA; 18 BP.
XX
AC   AAT50605;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #280.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 9 C; 4 G; 2 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 91;
  Matches  16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    274 ccagaccgccttccagcg 291
          ||||||||||::||||||
Db      1 ccagaccgccuuccagcg 18


RESULT  19
AAT50606
ID   AAT50606 standard; RNA; 18 BP.
XX
AC   AAT50606;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #369.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
```

PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 52; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 6 A; 7 C; 2 G; 3 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 363 acatccagatcagccact 380
||||:|||||:|||||||:
Db 1 acauccagaucagccacu 18

RESULT 20
AAT50607
ID AAT50607 standard; RNA; 18 BP.
XX
AC AAT50607;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #490.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 52; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 2 A; 7 C; 5 G; 4 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 484 caccactgcctggtggct 501
||||||:|||:||:|||:
Db 1 caccacugccuggguggcu 18

RESULT 21
AAT50608
ID AAT50608 standard; RNA; 18 BP.
XX
AC AAT50608;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #513.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.

XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 52; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 4 A; 4 C; 3 G; 7 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 61.1%; Pred. No. 91;
Matches 11; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 507 ttgatcagtccattgact 524
::||:|||:|||::|||:
Db 1 uugaucaguccauugacu 18

RESULT 22
AAT50609
ID AAT50609 standard; RNA; 18 BP.
XX
AC AAT50609;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #552.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 52; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 7 A; 8 C; 1 G; 2 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 546 acctccagatcaacacac 563
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Db 1 accuccagaucaacacac 18

RESULT 23
AAT50610
ID AAT50610 standard; RNA; 18 BP.
XX
AC AAT50610;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #564.

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XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 5 A; 6 C; 4 G; 3 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 91;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     558 acacacagctgacctgtg 575
           ||||||||:||||:|:|
Db       1 acacacagcugaccugug 18


RESULT  24
AAT50611
ID   AAT50611 standard; RNA; 18 BP.
XX
AC   AAT50611;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #567.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 52; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 4 A; 6 C; 4 G; 4 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     561 cacagctgacctgtgact 578
           ||||||:||||:|:|||:
Db       1 cacagcugaccugugacu 18
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RESULT  25
AAT50612
ID   AAT50612 standard; RNA; 18 BP.
XX
AC   AAT50612;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #591.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 6 C; 7 G; 2 U; 0 other;

  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 91;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     585 gagtgcggaccgatgccc 602
           |||:||||||||:||||
Db       1 gagugcggaccgaugccc 18


RESULT  26
AAT50613
ID   AAT50613 standard; RNA; 18 BP.
XX
AC   AAT50613;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #595.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 7 C; 6 G; 2 U; 0 other;
```

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy    589 gcggaccgatgcccctga 606
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Db      1 gcggaccgaugccccuga 18
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RESULT 27
AAT50614
ID AAT50614 standard; RNA; 18 BP.
XX
AC AAT50614;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #604.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 2 A; 8 C; 3 G; 5 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 72.2%; Pred. No. 91;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy    598 tgcccctgactgctacct 615
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Db      1 ugccccugacugcuaccu 18
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RESULT 28
AAT50615
ID AAT50615 standard; RNA; 18 BP.
XX
AC AAT50615;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #615.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular

```
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 6 C; 2 G; 7 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   61.1%;  Pred. No. 91;
  Matches   11;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     609 gctacctgtctttccata 626
           ||:|||:|:|:::|||:|
Db       1 gcuaccugucuuuccaua 18


RESULT  29
AAT50616
ID   AAT50616 standard; RNA; 18 BP.
XX
AC   AAT50616;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #630.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 4 A; 6 C; 3 G; 5 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 91;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     624 ataagctgctcctgcatc 641
           |:||||:||:||:|||:|
Db       1 auaagcugcuccugcauc 18


RESULT  30
AAT50617
ID   AAT50617 standard; RNA; 18 BP.
XX
AC   AAT50617;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #675.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
```

```
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 6 A; 5 C; 3 G; 4 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     669 tcaagcagctgttcacaa 686
           :|||||||||:|::|||||
Db       1 ucaagcagcuguucacaa 18


RESULT  31
AAT50618
ID   AAT50618 standard; RNA; 18 BP.
XX
AC   AAT50618;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #678.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 6 A; 4 C; 3 G; 5 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 91;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     672 agcagctgttcacaaatt 689
           ||||||:|::|||||::
Db       1 agcagcuguucacaaauu 18


RESULT  32
AAT50619
ID   AAT50619 standard; RNA; 18 BP.
XX
AC   AAT50619;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #726.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
```

PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 7 A; 3 C; 6 G; 2 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 720 agggacagatctgcaaag 737
||||||||||:|:||||||
Db 1 agggacagaucugcaaag 18

RESULT 33
AAT50620
ID AAT50620 standard; RNA; 18 BP.
XX
AC AAT50620;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #766.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 3 A; 5 C; 4 G; 6 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 760 catggccgattttgtcca 777
||:||||||::::|:|||
Db 1 cauggccgauuuugucca 18

RESULT 34
AAT50621
ID AAT50621 standard; RNA; 18 BP.
XX
AC AAT50621;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #802.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.

```
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 5 A; 4 C; 4 G; 5 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 91;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    796 cctttcagatggagacat 813
          ||:::||||:|||||||:
Db      1 ccuuucagauggagacau 18


RESULT  35
AAT50622
ID   AAT50622 standard; RNA; 18 BP.
XX
AC   AAT50622;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #853.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 4 A; 9 C; 1 G; 4 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    847 catcacagcctcctacct 864
          ||:|||||||:||:|||:
Db      1 caucacagccuccuaccu 18


RESULT  36
AAT50623
ID   AAT50623 standard; RNA; 18 BP.
XX
AC   AAT50623;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #942.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
```

XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 3 A; 6 C; 6 G; 3 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 936 ccacactgctgggggact 953
|||||||:||:|||||||:
Db 1 ccacacugcuggggacu 18

RESULT 37
AAT50624
ID AAT50624 standard; RNA; 18 BP.
XX
AC AAT50624;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #1025.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 2 A; 7 C; 5 G; 4 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1019 gatggccgcctcatgctc 1036
||:|||||||:||:||:|
Db 1 gauggccgccucaugcuc 18

RESULT 38
AAT50625
ID AAT50625 standard; RNA; 18 BP.
XX
AC AAT50625;
XX
DT 10-MAR-1997 (first entry)

XX
DE Human CETP hairpin ribozyme target sequence #1037.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 4 A; 4 C; 6 G; 4 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1031 atgctcagcctgatggga 1048
|:||:|||||:||:||||
Db 1 augcucagccugauggga 18

RESULT 39
AAT50743
ID AAT50743 standard; RNA; 18 BP.
XX
AC AAT50743;
XX
DT 07-MAR-1997 (first entry)
XX
DE Rabbit CETP hairpin ribozyme target sequence #1463.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
KW LDL; ss.
XX
OS Oryctolagus cuniculus.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 56; 72pp; English.
XX
CC AAT50699-T50754 represent target sequences for the rabbit cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50643-T50698).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 72.2%; Pred. No. 91;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1575 agcacctgctggtggatt 1592
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Db      1 agcaccugcugguggauu 18

RESULT  40
AAT50626
ID   AAT50626 standard; RNA; 18 BP.
XX
AC   AAT50626;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #1041.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 4 A; 4 C; 7 G; 3 U; 0 other;

 Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 91;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1035 tcagcctgatgggagacg 1052
           :|||||:||:||||||||
Db      1 ucagccugaugggagacg 18


RESULT  41
AAT50627
ID   AAT50627 standard; RNA; 18 BP.
XX
AC   AAT50627;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #1121.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
```

```
XX
SQ   Sequence 18 BP; 1 A; 8 C; 6 G; 3 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 91;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1115 gtcggcggcttccccagc 1132
           |:||||||::|||||||
Db      1 gucggcggcuuccccagc 18


RESULT  42
AAT50628
ID   AAT50628 standard; RNA; 18 BP.
XX
AC   AAT50628;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #1147.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
CC   peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC   familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC   complications of diabetes, transplant, atherectomy and angioplastic
CC   restenosis.  By inhibiting CETP, the levels of HDL and low density
CC   lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC   decrease in LDL levels, and a corresponding increase in HDL levels).  The
CC   ribozymes can also be used diagnostically to study genetic drift and
CC   mutations in diseased cells, and to detect CETP mRNA.  As the ribozymes
CC   target specific regions of the CETP gene, they have low non-specific
CC   activity.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 3 G; 4 U; 0 other;


  Query Match             1.0%;  Score 18;  DB 17;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1141 agtcaccgtccactgcct 1158
           ||:|||||:||||:|||:
Db      1 agucaccguccacugccu 18


RESULT  43
AAT50629
ID   AAT50629 standard; RNA; 18 BP.
XX
AC   AAT50629;
XX
DT   10-MAR-1997  (first entry)
XX
DE   Human CETP hairpin ribozyme target sequence #1154.
XX
KW   Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW   neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW   reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW   familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW   peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW   angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW   LDL; ss.
XX
OS   Homo sapiens.
XX
PN   WO9620279-A1.
XX
PD   04-JUL-1996.
XX
PF   11-DEC-1995;   95WO-US16000.
XX
PR   23-DEC-1994;   94US-0363240.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bisgaier C,  Couture L,  McSwiggen J,  Pape M,  Stinchcomb D;
XX
DR   WPI; 1996-321852/32.
XX
PT   New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT   - useful for preventing or treating initial development, progression
PT   or regression of vascular diseases, esp. familial
PT   hypercholesterolaemia
XX
PS   Claim 4; Page 53; 72pp; English.
XX
CC   AAT50595-T50642 represent target sequences for the human cholesterol
CC   ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC   CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC   between plasma lipoproteins.  The numbering of the targets refers to the
CC   position of the cleavage site in full length CETP.  The ribozyme then
CC   binds to 4-6 nucleotides 5', and a variable number 3' of this site.  The
CC   ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC   blocking synthesis and/or expression of the mRNA.  By inhibiting CETP,
CC   the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC   eliminated) thereby preventing the reduction in size density of the high
CC   density lipoproteins (HDL), prolonging HDL half life, and therefore
CC   increasing HDL levels.  The ribozymes can be used to treat conditions
CC   associated with abnormal levels of CETP, specifically atherosclerosis,
```

CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 4 A; 6 C; 4 G; 4 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 gtccactgcctcaagatg 1165
|:||||:|||:|||||:|
Db 1 guccacugccucaagaug 18

RESULT 44
AAT50630
ID AAT50630 standard; RNA; 18 BP.
XX
AC AAT50630;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #1240.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 7 A; 8 C; 3 G; 0 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1234 acgcccagaccagcaaca 1251
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Db 1 acgcccagaccagcaaca 18

RESULT 45
AAT50631
ID AAT50631 standard; RNA; 18 BP.
XX
AC AAT50631;
XX
DT 10-MAR-1997 (first entry)
XX
DE Human CETP hairpin ribozyme target sequence #1291.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US16000.
XX
PR 23-DEC-1994; 94US-0363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT - useful for preventing or treating initial development, progression
PT or regression of vascular diseases, esp. familial
PT hypercholesterolaemia
XX
PS Claim 4; Page 53; 72pp; English.
XX
CC AAT50595-T50642 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer

CC between plasma lipoproteins. The numbering of the targets refers to the
CC position of the cleavage site in full length CETP. The ribozyme then
CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC eliminated) thereby preventing the reduction in size density of the high
CC density lipoproteins (HDL), prolonging HDL half life, and therefore
CC increasing HDL levels. The ribozymes can be used to treat conditions
CC associated with abnormal levels of CETP, specifically atherosclerosis,
CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CETP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
CC target specific regions of the CETP gene, they have low non-specific
CC activity.
XX
SQ Sequence 18 BP; 3 A; 8 C; 4 G; 3 U; 0 other;

Query Match 1.0%; Score 18; DB 17; Length 18;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1285 gactaccgtccaggcctc 1302
||||:||||:|||||||:|
Db 1 gacuaccguccaggccuc 18

Search completed: April 20, 2002, 01:13:33
Job time: 4465 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2002, 22:03:21 ; Search time 92.54 Seconds
(without alignments)
4373.419 Million cell updates/sec

Title: US-09-925-139-3
Perfect score: 1787
Sequence: 1 gtgaatctctggggccagga.....ggcattaaagtgctgtatcc 1787

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : 0

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	2.6	46	1	US-08-171-389-89	Sequence 89, Appl
2	46	2.6	46	1	US-08-123-936-89	Sequence 89, Appl
3	46	2.6	46	2	US-08-475-228A-89	Sequence 89, Appl
4	46	2.6	46	3	US-08-482-080A-89	Sequence 89, Appl
5	46	2.6	46	5	PCT-US93-12388-89	Sequence 89, Appl
6	18	1.0	18	1	US-08-363-240A-1078	Sequence 1078, Ap
7	18	1.0	18	1	US-08-363-240A-1079	Sequence 1079, Ap
8	18	1.0	18	1	US-08-363-240A-1080	Sequence 1080, Ap
9	18	1.0	18	1	US-08-363-240A-1081	Sequence 1081, Ap
10	18	1.0	18	1	US-08-363-240A-1082	Sequence 1082, Ap
11	18	1.0	18	1	US-08-363-240A-1083	Sequence 1083, Ap
12	18	1.0	18	1	US-08-363-240A-1084	Sequence 1084, Ap
13	18	1.0	18	1	US-08-363-240A-1085	Sequence 1085, Ap
14	18	1.0	18	1	US-08-363-240A-1086	Sequence 1086, Ap
15	18	1.0	18	1	US-08-363-240A-1087	Sequence 1087, Ap
16	18	1.0	18	1	US-08-363-240A-1088	Sequence 1088, Ap
17	18	1.0	18	1	US-08-363-240A-1089	Sequence 1089, Ap
18	18	1.0	18	1	US-08-363-240A-1090	Sequence 1090, Ap
19	18	1.0	18	1	US-08-363-240A-1091	Sequence 1091, Ap
20	18	1.0	18	1	US-08-363-240A-1092	Sequence 1092, Ap
21	18	1.0	18	1	US-08-363-240A-1093	Sequence 1093, Ap
22	18	1.0	18	1	US-08-363-240A-1094	Sequence 1094, Ap
23	18	1.0	18	1	US-08-363-240A-1095	Sequence 1095, Ap
24	18	1.0	18	1	US-08-363-240A-1096	Sequence 1096, Ap
25	18	1.0	18	1	US-08-363-240A-1097	Sequence 1097, Ap
26	18	1.0	18	1	US-08-363-240A-1098	Sequence 1098, Ap
27	18	1.0	18	1	US-08-363-240A-1099	Sequence 1099, Ap
28	18	1.0	18	1	US-08-363-240A-1100	Sequence 1100, Ap
29	18	1.0	18	1	US-08-363-240A-1101	Sequence 1101, Ap
30	18	1.0	18	1	US-08-363-240A-1102	Sequence 1102, Ap
31	18	1.0	18	1	US-08-363-240A-1103	Sequence 1103, Ap
32	18	1.0	18	1	US-08-363-240A-1104	Sequence 1104, Ap
33	18	1.0	18	1	US-08-363-240A-1105	Sequence 1105, Ap
34	18	1.0	18	1	US-08-363-240A-1106	Sequence 1106, Ap
35	18	1.0	18	1	US-08-363-240A-1107	Sequence 1107, Ap
36	18	1.0	18	1	US-08-363-240A-1108	Sequence 1108, Ap
37	18	1.0	18	1	US-08-363-240A-1109	Sequence 1109, Ap
38	18	1.0	18	1	US-08-363-240A-1110	Sequence 1110, Ap
39	18	1.0	18	1	US-08-363-240A-1111	Sequence 1111, Ap
40	18	1.0	18	1	US-08-363-240A-1112	Sequence 1112, Ap
41	18	1.0	18	1	US-08-363-240A-1113	Sequence 1113, Ap
42	18	1.0	18	1	US-08-363-240A-1114	Sequence 1114, Ap
43	18	1.0	18	1	US-08-363-240A-1115	Sequence 1115, Ap
44	18	1.0	18	1	US-08-363-240A-1116	Sequence 1116, Ap
45	18	1.0	18	1	US-08-363-240A-1117	Sequence 1117, Ap

ALIGNMENTS

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RESULT 1
US-08-171-389-89
; Sequence 89, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
;   APPLICANT: Edwards, Cynthia A.
;   APPLICANT: Cantor, Charles R.
;   APPLICANT: Andrews, Beth M.
;   APPLICANT: Turin, Lisa M.
;   APPLICANT: Fry, Kirk E.
;   TITLE OF INVENTION: Sequence-Directed DNA Binding
;   TITLE OF INVENTION: Molecules, Compositions and Methods
;   NUMBER OF SEQUENCES: 641
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genelabs Technologies, Inc.
;     STREET: 505 Penobscot Drive
;     CITY: Redwood City
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94063
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/171,389
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/123,936
;     FILING DATE: 17-SEP-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/996,783
;     FILING DATE: 23-DEC-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/723,618
;     FILING DATE: 27-JUN-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/081,070
;     FILING DATE: 22-JUN-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fabian, Gary R.
;     REGISTRATION NUMBER: 33,875
;     REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 324-0880
;     TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 89:
;   SEQUENCE CHARACTERISTICS:
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;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human cholesteryl ester transferase
;      INDIVIDUAL ISOLATE:  protein (CETP) gene
US-08-171-389-89


  Query Match             2.6%;  Score 46;  DB 1;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-13;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
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Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   2
US-08-123-936-89
; Sequence 89, Application US/08123936
; Patent No. 5726014
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    TITLE OF INVENTION:  Screening Assay for the Detection of
;    TITLE OF INVENTION:  DNA-Binding Molecules
;    NUMBER OF SEQUENCES:  640
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/123,936
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0075.32/G19P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human cholesteryl ester transferase
;      INDIVIDUAL ISOLATE:  protein (CETP) gene

US-08-123-936-89


  Query Match             2.6%;  Score 46;  DB 1;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-13;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
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Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   3
US-08-475-228A-89
; Sequence 89, Application US/08475228A
; Patent No. 5869241
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,228A
;      FILING DATE:  06-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stratford, Carol A.
;      REGISTRATION NUMBER:  34,444
;      REFERENCE/DOCKET NUMBER:  4600-0175.21/G19P3D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human cholesteryl ester transferase
;      INDIVIDUAL ISOLATE:  protein (CETP) gene
US-08-475-228A-89
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  Query Match              2.6%;  Score 46;  DB 2;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-13;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   4
US-08-482-080A-89
; Sequence 89, Application US/08482080A
; Patent No. 6010849
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,080A
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/171,389
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brady, John F.
;      REGISTRATION NUMBER:  39,118
;      REFERENCE/DOCKET NUMBER:  4600-0175.20/G19P3D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human cholesteryl ester transferase
;      INDIVIDUAL ISOLATE:  protein (CETP) gene
US-08-482-080A-89


  Query Match              2.6%;  Score 46;  DB 3;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-13;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
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Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   5
PCT-US93-12388-89
; Sequence 89, Application PC/TUS9312388
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12388
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0175.41/G19PCT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human cholesteryl ester transferase
;      INDIVIDUAL ISOLATE:  protein (CETP) gene
PCT-US93-12388-89


  Query Match              2.6%;  Score 46;  DB 5;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-13;
  Matches   46;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 gtgggggctgggcggacatacatatacgggctccaggctgaacggc 98
           ||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGGGGGCTGGGCGGACATACATATACGGGCTCCAGGCTGAACGGC 46


RESULT   6
US-08-363-240A-1078
; Sequence 1078, Application US/08363240A
; Patent No. 5705388
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;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1078:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1078


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 agaccctgctgcccggaa 38
           ||||||:||:||||||||
Db       1 AGACCCUGCUGCCCGGAA 18


RESULT   7
US-08-363-240A-1079
; Sequence 1079, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1079:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1079


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      24 ccctgctgcccggaagag 41
           |||:||:||||||||||
Db       1 CCCUGCUGCCCGGAAGAG 18


RESULT   8
US-08-363-240A-1080
; Sequence 1080, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
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;       FILING DATE:  December 23, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1080:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1080


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      90 ctgaacggctcgggccac 107
           |:|||||||:||||||||
Db       1 CUGAACGGCUCGGGCCAC 18


RESULT   9
US-08-363-240A-1081
; Sequence 1081, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1081:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1081


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     113 caccactgcctgataacc 130
           ||||||:|||:||:||||
Db       1 CACCACUGCCUGAUAACC 18


RESULT  10
US-08-363-240A-1082
; Sequence 1082, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1082:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1082


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     139 tgccacagtcctgaccct 156
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              :||||||||:||:||||||:
Db         1 UGCCACAGUCCUGACCCU 18


RESULT  11
US-08-363-240A-1083
; Sequence 1083, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1083:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1083


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     144 cagtcctgaccctggccc 161
           |||:||:|||||:|||||
Db       1 CAGUCCUGACCCUGGCCC 18


RESULT  12
US-08-363-240A-1084
; Sequence 1084, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1084:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1084


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     156 tggccctgctgggcaatg 173
           :|||||:||:|||||||:|
Db       1 UGGCCCUGCUGGGCAAUG 18


RESULT  13
US-08-363-240A-1085
; Sequence 1085, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1085:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1085


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     176 catgcctgctccaaaggc 193
           ||:|||:||:||||||||
Db       1 CAUGCCUGCUCCAAAGGC 18


RESULT  14
US-08-363-240A-1086
; Sequence 1086, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1086:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1086


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     229 caagcctgccctcctggt 246
           ||||||:||||:||:||:
Db       1 CAAGCCUGCCCUCCUGGU 18


RESULT  15
US-08-363-240A-1087
; Sequence 1087, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1087:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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US-08-363-240A-1087

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy    270 tgatccagaccgccttcc 287
          :||:||||||||||::||
Db      1 UGAUCCAGACCGCCUUCC 18
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RESULT 16
US-08-363-240A-1088
; Sequence 1088, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1088:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-1088

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy    274 ccagaccgccttccagcg 291
          ||||||||||::||||||
Db      1 CCAGACCGCCUUCCAGCG 18
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RESULT 17
US-08-363-240A-1089
; Sequence 1089, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1089:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-1089

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy    363 acatccagatcagccact 380
          |||:||||||:|||||||:
Db      1 ACAUCCAGAUCAGCCACU 18
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RESULT 18
US-08-363-240A-1090
; Sequence 1090, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1090:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1090


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     484 caccactgcctggtggct 501
           ||||||:|||:||:|||:
Db       1 CACCACUGCCUGGUGGCU 18


RESULT  19
US-08-363-240A-1091
; Sequence 1091, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1091:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1091


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   61.1%;  Pred. No. 26;
  Matches   11;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     507 ttgatcagtccattgact 524
           ::||:|||:|||::|||:
Db       1 UUGAUCAGUCCAUUGACU 18


RESULT  20
US-08-363-240A-1092
; Sequence 1092, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
```

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;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1092:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1092


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     546 acctccagatcaacacac 563
           |||:||||||:||||||||
Db       1 ACCUCCAGAUCAACACAC 18


RESULT  21
US-08-363-240A-1093
; Sequence 1093, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1093:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1093


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     558 acacacagctgacctgtg 575
           ||||||||:||||:|:|
Db       1 ACACACAGCUGACCUGUG 18


RESULT  22
US-08-363-240A-1094
; Sequence 1094, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1094:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1094


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     561 cacagctgacctgtgact 578
           ||||||:||||:|:|||:
Db       1 CACAGCUGACCUGUGACU 18


RESULT  23
US-08-363-240A-1095
; Sequence 1095, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
```

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;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1095:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1095


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     585 gagtgcggaccgatgccc 602
           |||:||||||||||:||||
Db       1 GAGUGCGGACCGAUGCCC 18


RESULT  24
US-08-363-240A-1096
; Sequence 1096, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1096:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1096


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     589 gcggaccgatgcccctga 606
           |||||||||:|||||:||
Db       1 GCGGACCGAUGCCCCUGA 18


RESULT  25
US-08-363-240A-1097
; Sequence 1097, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1097:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1097


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 26;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    598 tgcccctgactgctacct 615
          :|||||:|||:||:|||:
Db      1 UGCCCCUGACUGCUACCU 18


RESULT  26
US-08-363-240A-1098
; Sequence 1098, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1098:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1098


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   61.1%;  Pred. No. 26;
  Matches   11;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    609 gctacctgtctttccata 626
          ||:|||:|:|:::|||:|
Db      1 GCUACCUGUCUUUCCAUA 18


RESULT  27
US-08-363-240A-1099
; Sequence 1099, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1099:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1099


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 26;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    624 ataagctgctcctgcatc 641
          |:||||:||:||:|||:|
Db      1 AUAAGCUGCUCCUGCAUC 18
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RESULT  28
US-08-363-240A-1100
; Sequence 1100, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1100


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    669 tcaagcagctgttcacaa 686
          :|||||||||:|::|||||
Db      1 UCAAGCAGCUGUUCACAA 18


RESULT  29
US-08-363-240A-1101
; Sequence 1101, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1101:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1101


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 26;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    672 agcagctgttcacaaatt 689
          ||||||:|::||||||::
Db      1 AGCAGCUGUUCACAAAUU 18


RESULT  30
US-08-363-240A-1102
; Sequence 1102, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
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;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1102:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1102


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 26;
  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    720 agggacagatctgcaaag 737
          |||||||||:|:||||||
Db      1 AGGGACAGAUCUGCAAAG 18


RESULT  31
US-08-363-240A-1103
; Sequence 1103, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1103


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 26;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    760 catggccgattttgtcca 777
          ||:||||||::::|:|||
Db      1 CAUGGCCGAUUUUGUCCA 18


RESULT  32
US-08-363-240A-1104
; Sequence 1104, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1104
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  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 26;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     796 cctttcagatggagacat 813
           ||:::||||:|||||||:
Db       1 CCUUUCAGAUGGAGACAU 18


RESULT  33
US-08-363-240A-1105
; Sequence 1105, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1105


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     847 catcacagcctcctacct 864
           ||:|||||||:||:|||:
Db       1 CAUCACAGCCUCCUACCU 18


RESULT  34
US-08-363-240A-1106
; Sequence 1106, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1106:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1106


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     936 ccacactgctgggggact 953
           ||||||:||:|||||||:
Db       1 CCACACUGCUGGGGGACU 18


RESULT  35
US-08-363-240A-1107
; Sequence 1107, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-1107

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1019 gatggccgcctcatgctc 1036
||:|||||||:||:||:|
Db 1 GAUGGCCGCCUCAUGCUC 18

RESULT 36
US-08-363-240A-1108
; Sequence 1108, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-1108

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1031 atgctcagcctgatggga 1048
|:||:|||||:||:||||
Db 1 AUGCUCAGCCUGAUGGGA 18

RESULT 37
US-08-363-240A-1109
; Sequence 1109, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

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;  INFORMATION FOR SEQ ID NO:  1109:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1109


  Query Match           1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1035 tcagcctgatgggagacg 1052
          :|||||:||:||||||||
Db      1 UCAGCCUGAUGGGAGACG 18


RESULT  38
US-08-363-240A-1110
; Sequence 1110, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1110:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1110


  Query Match           1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1115 gtcggcggcttccccagc 1132
          |:|||||||::|||||||
Db      1 GUCGGCGGCUUCCCCAGC 18


RESULT  39
US-08-363-240A-1111
; Sequence 1111, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1111:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1111


  Query Match           1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1141 agtcaccgtccactgcct 1158
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Db      1 AGUCACCGUCCACUGCCU 18


RESULT  40
US-08-363-240A-1112
; Sequence 1112, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
```

```
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1112


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 26;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1148 gtccactgcctcaagatg 1165
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RESULT  41
US-08-363-240A-1113
; Sequence 1113, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1113


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1234 acgcccagaccagcaaca 1251
          ||||||||||||||||||
Db      1 ACGCCCAGACCAGCAACA 18


RESULT  42
US-08-363-240A-1114
; Sequence 1114, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
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;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1114:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1114


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 26;
  Matches   15;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1285 gactaccgtccaggcctc 1302
           |||:||||:|||||||:|
Db       1 GACUACCGUCCAGGCCUC 18


RESULT  43
US-08-363-240A-1115
; Sequence 1115, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;     APPLICANT:  Couture, Larry
;     APPLICANT:  McSwiggen, James
;     APPLICANT:  Bisgaier, Charles
;     APPLICANT:  Pape, Michael
;     TITLE OF INVENTION:  METHOD AND REAGENT FOR
;     TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;     TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;     TITLE OF INVENTION:  OF VASCULAR DISEASES
;     NUMBER OF SEQUENCES:  1243
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Lyon & Lyon
;       STREET:  633 West Fifth Street
;       STREET:  Suite 4700
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/363,240A
;       FILING DATE:  December 23, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1115:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1115


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  Best Local Similarity   72.2%;  Pred. No. 26;
  Matches   13;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1338 atttccagattacaccaa 1355
           |:::|||||::|||||||
Db       1 AUUUCCAGAUUACACCAA 18


RESULT  44
US-08-363-240A-1116
; Sequence 1116, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;     APPLICANT:  Couture, Larry
;     APPLICANT:  McSwiggen, James
;     APPLICANT:  Bisgaier, Charles
;     APPLICANT:  Pape, Michael
;     TITLE OF INVENTION:  METHOD AND REAGENT FOR
;     TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;     TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;     TITLE OF INVENTION:  OF VASCULAR DISEASES
;     NUMBER OF SEQUENCES:  1243
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Lyon & Lyon
;       STREET:  633 West Fifth Street
;       STREET:  Suite 4700
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/363,240A
;       FILING DATE:  December 23, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  1116:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1116


  Query Match             1.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 26;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1354 aaagactgtttccaactt 1371
           ||||||:|:::||||||::
Db       1 AAAGACUGUUUCCAACUU 18
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```
RESULT  45
US-08-363-240A-1117
; Sequence 1117, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;     APPLICANT:  Couture, Larry
;     APPLICANT:  McSwiggen, James
;     APPLICANT:  Bisgaier, Charles
;     APPLICANT:  Pape, Michael
;     TITLE OF INVENTION:  METHOD AND REAGENT FOR
;     TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;     TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;     TITLE OF INVENTION:  OF VASCULAR DISEASES
;     NUMBER OF SEQUENCES:  1243
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Lyon & Lyon
;       STREET:  633 West Fifth Street
;       STREET:  Suite 4700
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
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;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/363,240A
;       FILING DATE:  December 23, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1117:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-1117


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  Matches   16;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 GAGAGCAGCUCCGAGUCC 18


Search completed: April 20, 2002, 01:10:12
Job time: 11211 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 19, 2002, 21:54:56 ; Search time 1541.31 Seconds
(without alignments)
12458.692 Million cell updates/sec

Title: US-09-925-139-3
Perfect score: 1787
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

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Total number of hits satisfying chosen parameters: 80718

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
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8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
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16: em_gss_inv:*
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18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	0.8	43	10	AI014286	AI014286 am46a02.s
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3	14	0.8	19	13	AZ510143	AZ510143 1M0354P21
c 4	14	0.8	31	13	AZ979245	AZ979245 2M0255D20
c 5	14	0.8	37	10	AA995811	AA995811 os05e12.s
c 6	14	0.8	43	13	AZ595978	AZ595978 1M0408O23
c 7	14	0.8	47	13	AZ827718	AZ827718 2M0104M16
8	14	0.8	48	10	AI215970	AI215970 qh06g04.x
9	14	0.8	48	13	AZ834843	AZ834843 2M0117E18
c 10	14	0.8	49	13	TA3D11Q	AL451995 T. brucei
c 11	14	0.8	50	10	AI252059	AI252059 qv39f04.x
12	14	0.8	50	10	AU104702	AU104702 AU104702
13	13	0.7	19	10	AI027323	AI027323 ow46a07.s
c 14	13	0.7	19	13	AZ792979	AZ792979 2M0046G04
c 15	13	0.7	22	10	AA959224	AA959224 ua10h06.r
16	13	0.7	22	13	AZ830573	AZ830573 2M0109G23
17	13	0.7	23	13	AZ499076	AZ499076 1M0336H08
c 18	13	0.7	24	13	AZ820462	AZ820462 2M0092H02
c 19	13	0.7	26	13	AZ377014	AZ377014 1M0131F08
c 20	13	0.7	27	13	AZ621737	AZ621737 1M0455F15
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23	13	0.7	31	10	AA867755	AA867755 vx16b08.r
c 24	13	0.7	31	13	AZ777749	AZ777749 2M0012H13
c 25	13	0.7	31	13	AZ938547	AZ938547 2M0197J10
26	13	0.7	32	13	AZ618214	AZ618214 1M0449O16
27	13	0.7	34	10	AA920912	AA920912 vy84f09.r
28	13	0.7	35	13	AZ469734	AZ469734 1M0283J19
c 29	13	0.7	36	13	AZ825411	AZ825411 2M0100A09
30	13	0.7	37	10	AA978054	AA978054 oq55h01.s
31	13	0.7	39	13	AZ663277	AZ663277 1M0542O15
c 32	13	0.7	39	13	AZ781715	AZ781715 2M0021F16
c 33	13	0.7	39	13	AZ825536	AZ825536 2M0100J14
34	13	0.7	40	10	AA680336	AA680336 ac83e09.s
35	13	0.7	40	10	AI001093	AI001093 os94c01.s
c 36	13	0.7	42	10	BE383987	BE383987 601273364
37	13	0.7	44	10	AA922988	AA922988 ok77f09.s
38	13	0.7	44	11	T48887	T48887 yb07a05.r1
c 39	13	0.7	44	13	AZ498888	AZ498888 1M0336E21
c 40	13	0.7	45	13	AZ480635	AZ480635 1M0302M18
41	13	0.7	46	10	AA730149	AA730149 nx38f03.s
42	13	0.7	46	10	AA902889	AA902889 oj49g04.s
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44	13	0.7	46	10	AI264859	AI264859 qx66h12.x
c 45	13	0.7	46	10	AI439347	AI439347 ti54f06.x

ALIGNMENTS

RESULT 1
AI014286
LOCUS AI014286 43 bp mRNA EST 15-JUN-1998
DEFINITION am46a02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538570 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA sequence.
ACCESSION AI014286
VERSION AI014286.1 GI:3228118
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IMAGE:1538570"
/clone_lib="Johnston frontal cortex"
/sex="male"
/tissue_type="pooled frontal lobe"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site_1: EcoRI ; Stanley Neuropathology Consortium (www.stanleylab.org) brains S-58, S-65, S-67, S-78. Random + oligo-dT primed into EcoRI site of ZAP II Vector. Mass excised. Avg insert length 1.9kb. Custom library provided by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]. "

BASE COUNT 5 a 15 c 13 g 10 t
ORIGIN

Query Match 0.8%; Score 15; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 atctctggggccagg 19
||||||||||||||||
Db 5 ATCTCTGGGGCCAGG 19

RESULT .2
AZ512770/c
LOCUS AZ512770 44 bp DNA GSS 05-OCT-2000
DEFINITION 1M0358O02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0358O02 R, DNA sequence.
ACCESSION AZ512770
VERSION AZ512770.1 GI:10694086
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 44)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0358 row: O column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 44.
FEATURES Location/Qualifiers
source 1. .44
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0358O02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 14 c 3 g 15 t
ORIGIN

Query Match 0.8%; Score 15; DB 13; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 392 agcagccaggtggag 406
||||||||||||||||
Db 37 AGCAGCCAGGTGGAG 23

RESULT 3
AZ510143
LOCUS AZ510143 19 bp DNA GSS 05-OCT-2000
DEFINITION 1M0354P21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0354P21 F, DNA sequence.
ACCESSION AZ510143
VERSION AZ510143.1 GI:10691459
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: P column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354P21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 13 c 0 g 2 t
ORIGIN

Query Match 0.8%; Score 14; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 915 tccccctccccacc 928
||||||||||||||
Db 5 TCCCCCTCCCCACC 18

RESULT 4
AZ979245/c
LOCUS AZ979245 31 bp DNA GSS 27-APR-2001
DEFINITION 2M0255D20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0255D20 R, DNA sequence.
ACCESSION AZ979245
VERSION AZ979245.1 GI:13850472
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0255 row: D column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
FEATURES Location/Qualifiers
source 1. .31
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0255D20"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 3 c 16 g 4 t
ORIGIN

Query Match 0.8%; Score 14; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.9e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 915 tccccctccccacc 928
||||||||||||||
Db 30 TCCCCCTCCCCACC 17

RESULT 5
AA995811/c
LOCUS AA995811 37 bp mRNA EST 27-JUL-1998
DEFINITION os05e12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1604494 3' similar to WP:C47D12.2 CE05430 ;, mRNA sequence.
ACCESSION AA995811
VERSION AA995811.1 GI:3182300
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.; Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1425 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1604494"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated

to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 12 a 5 c 8 g 12 t
ORIGIN

Query Match 0.8%; Score 14; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 749 atctctaacatcat 762
||||||||||||||
Db 27 ATCTCTAACATCAT 14

RESULT 6
AZ595978/c
LOCUS AZ595978 43 bp DNA GSS 13-DEC-2000
DEFINITION 1M0408O23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0408O23 R, DNA sequence.
ACCESSION AZ595978
VERSION AZ595978.1 GI:11718168
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0408 row: O column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
FEATURES Location/Qualifiers
source 1. .43
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0408O23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 11 a 1 c 18 g 13 t
ORIGIN

Query Match 0.8%; Score 14; DB 13; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1738 cccaactcctccct 1751
||||||||||||||
Db 39 CCCAACTCCTCCCT 26

RESULT 7
AZ827718/c
LOCUS AZ827718 47 bp DNA GSS 20-FEB-2001
DEFINITION 2M0104M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0104M16 F, DNA sequence.
ACCESSION AZ827718
VERSION AZ827718.1 GI:12997626
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 47)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: M column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 47.
FEATURES Location/Qualifiers
source 1. .47
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0104M16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 15 a 13 c 7 g 12 t
ORIGIN

Query Match 0.8%; Score 14; DB 13; Length 47;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1301 tcctattctaagaa 1314
||||||||||||||
Db 33 TCCTATTCTAAGAA 20

RESULT 8
AI215970
LOCUS AI215970 48 bp mRNA EST 30-NOV-1998
DEFINITION qh06g04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843926 3' similar to gb:M68516_rna1 PLASMA SERINE PROTEASE (HUMAN);, mRNA sequence.
ACCESSION AI215970
VERSION AI215970.1 GI:3785011
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 3306 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .48
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1843926"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 13 a 17 c 4 g 14 t
ORIGIN

Query Match 0.8%; Score 14; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1127 cccagccaggccca 1140
||||||||||||||
Db 11 CCCAGCCAGGCCCA 24

RESULT 9
AZ834843
LOCUS AZ834843 48 bp DNA GSS 20-FEB-2001
DEFINITION 2M0117E18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0117E18 R, DNA sequence.
ACCESSION AZ834843
VERSION AZ834843.1 GI:13004751
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 48)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: E column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
FEATURES Location/Qualifiers
source 1. .48
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0117E18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 14 a 14 c 9 g 11 t
ORIGIN

Query Match 0.8%; Score 14; DB 13; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1755 ctaaaggcccactg 1768
          ||||||||||||||
Db     12 CTAAAGGCCCACTG 25


RESULT  10
TA3D11Q/c
LOCUS       TA3D11Q        49 bp    DNA             GSS       13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 3d11, reverse sequence, genomic
            survey sequence.
ACCESSION   AL451995
VERSION     AL451995.1  GI:11854310
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .49
                      /organism="Trypanosoma brucei"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="3d11"
BASE COUNT       13 a     19 c      9 g      8 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 13;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1546 gctgctgcagatgg 1559
          ||||||||||||||
Db     16 GCTGCTGCAGATGG 3


RESULT  11
AI252059/c
LOCUS       AI252059       50 bp    mRNA            EST       03-FEB-1999
DEFINITION  qv39f04.x1 NCI_CGAP_Ov31 Homo sapiens cDNA clone IMAGE:1983967 3'
            similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN);contains
            PTR5.t3 MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AI252059
VERSION     AI252059.1  GI:3848588
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Insert Length: 304   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .50
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1983967"
                      /clone_lib="NCI_CGAP_Ov31"
                      /sex="female"
                      /tissue_type="papillary serous carcinoma"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian
                      carcinoma, cDNA made by oligo-dT priming.
                      Non-directionally cloned. Size-selected on agarose gel,
                      average insert  size 500 bp.  Non-amplified library.  "
BASE COUNT       18 a      2 c     26 g      4 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 10;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    919 cctccccaccttct 932
          ||||||||||||||
Db     21 CCTCCCCACCTTCT 8


RESULT  12
AU104702
LOCUS       AU104702       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU104702 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC06060, mRNA sequence.
ACCESSION   AU104702
VERSION     AU104702.1  GI:13554223
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES              Location/Qualifiers
     source           1. .50
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="HRC06060"
                      /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT        4 a     23 c     17 g      6 t
ORIGIN


  Query Match             0.8%;  Score 14;  DB 10;  Length 50;
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  Best Local Similarity   100.0%;  Pred. No. 7.3e+04;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1125 tccccagccaggcc 1138
          ||||||||||||||
Db     32 TCCCCAGCCAGGCC 45


RESULT  13
AI027323
LOCUS       AI027323       19 bp    mRNA            EST       28-AUG-1998
DEFINITION  ow46a07.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:1649844 3' similar to TR:Q15929 Q15929 DNA-BINDING PROTEIN ;,
            mRNA sequence.
ACCESSION   AI027323
VERSION     AI027323.1  GI:3244839
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 968   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1649844"
                      /clone_lib="Soares_parathyroid_tumor_NbHPA"
                      /tissue_type="parathyroid tumor"
                      /dev_stage="adult"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia
                      ) with a modified polylinker; Site_1: Not I; Site_2: Eco
                      RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                      primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                      TTTTT-3'], double-stranded cDNA was size selected, ligated
                      to Eco RI adapters (Pharmacia), digested with Not I and
                      cloned into the Not I and Eco RI sites of a modified pT7T3
                      vector (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by Bento
                      Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                      adenomas was kindly provided by Dr. Stephen Marx, National
                      Institute of Diabetes and Digestive and Kidney Diseases,
                      NIH."
BASE COUNT        6 a      7 c      6 g      0 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    310 cacgggcgagaag 322
          |||||||||||||

Db      4 CACGGGCGAGAAG 16


RESULT  14
AZ792979/c
LOCUS       AZ792979       19 bp    DNA             GSS       16-FEB-2001
DEFINITION  2M0046G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0046G04 F, DNA sequence.
ACCESSION   AZ792979
VERSION     AZ792979.1  GI:12937658
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg.; 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0046  row: G  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0046G04"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        8 a      2 c      4 g      5 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    615 tgtctttccataa 627
```

```
              ||||||||||||||
Db      16 TGTCTTTCCATAA 4


RESULT  15
AA959224/c
LOCUS       AA959224       22 bp    mRNA            EST       08-MAY-1998
DEFINITION  ua10h06.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGE:1346363 5' similar to SW:COX3_MOUSE P00416 CYTOCHROME C
            OXIDASE POLYPEPTIDE III ;, mRNA sequence.
ACCESSION   AA959224
VERSION     AA959224.1  GI:3124417
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:695155
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1346363"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
                     ) with a modified polylinker; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT        8 a      7 c      2 g      5 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1215 tggtgaaattcct 1227
           |||||||||||||
Db     13 TGGTGAAATTCCT 1


RESULT  16
AZ830573
LOCUS       AZ830573       22 bp    DNA             GSS       20-FEB-2001
DEFINITION  2M0109G23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0109G23 R, DNA sequence.
ACCESSION   AZ830573
VERSION     AZ830573.1  GI:13000481
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0109  row: G  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0109G23"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        8 a      5 c      5 g      4 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1263 acacatttgaaga 1275
           |||||||||||||
Db      9 ACACATTTGAAGA 21
```

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RESULT  17
AZ499076
LOCUS       AZ499076       23 bp    DNA             GSS       05-OCT-2000
DEFINITION  1M0336H08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0336H08 R, DNA sequence.
ACCESSION   AZ499076
VERSION     AZ499076.1  GI:10677540
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0336  row: H  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0336H08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      16 c       1 g       6 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps  .  0;

Qy    913 cctccccctcccc 925
          |||||||||||||
```

```
Db      8 CCTCCCCCTCCCC 20


RESULT  18
AZ820462/c
LOCUS       AZ820462       24 bp    DNA             GSS       20-FEB-2001
DEFINITION  2M0092H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0092H02 R, DNA sequence.
ACCESSION   AZ820462
VERSION     AZ820462.1  GI:12990286
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0092  row: H  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0092H02"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        5 a       3 c       6 g      10 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     67 gacatacatatac 79
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          ||||||||||||||
Db      23 GACATACATATAC 11


RESULT 19
AZ377014/c
LOCUS       AZ377014        26 bp    DNA              GSS       02-OCT-2000
DEFINITION  1M0131F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0131F08 F, DNA sequence.
ACCESSION   AZ377014
VERSION     AZ377014.1  GI:10490714
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0131  row: F  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0131F08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        4 a      7 c      6 g      9 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     832 gacaggtgatccc 844
           |||||||||||||
Db      21 GACAGGTGATCCC 9


RESULT 20
AZ621737/c
LOCUS       AZ621737        27 bp    DNA              GSS       13-DEC-2000
DEFINITION  1M0455F15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0455F15 F, DNA sequence.
ACCESSION   AZ621737
VERSION     AZ621737.1  GI:11744023
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0455  row: F  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0455F15"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      3 c     10 g      8 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy    1513 caaccctgagatt 1525
           |||||||||||||
Db      27 CAACCCTGAGATT 15


RESULT  21
AZ783172
LOCUS       AZ783172       30 bp    DNA              GSS       16-FEB-2001
DEFINITION  2M0024F08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0024F08 R, DNA sequence.
ACCESSION   AZ783172
VERSION     AZ783172.1  GI:12917634
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0024  row: F  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0024F08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      27 c       0 g       3 t
ORIGIN


  Query Match              0.7%;  Score 13;  DB 13;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    913 cctccccctcccc 925
          |||||||||||||
Db     18 CCTCCCCCTCCCC 30


RESULT  22
AA865448
LOCUS       AA865448       31 bp    mRNA             EST       29-APR-1998
DEFINITION  oh50a06.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1470034 3'
            similar to SW:ROG_HUMAN P38159 HETEROGENEOUS NUCLEAR
            RIBONUCLEOPROTEIN G ;, mRNA sequence.
ACCESSION   AA865448
VERSION     AA865448.1  GI:2957724
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 753   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1470034"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        6 a      5 c      13 g       7 t
ORIGIN


  Query Match              0.7%;  Score 13;  DB 10;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1447 gtctcggctcgag 1459
          |||||||||||||
Db     14 GTCTCGGCTCGAG 26


RESULT  23
AA867755
LOCUS       AA867755       31 bp    mRNA             EST       16-MAR-1998
DEFINITION  vx16b08.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
```

```
            IMAGE:1264599 5' similar to TR:O35394 O35394 PRENYLATED RAB
            ACCEPTOR 1. ;, mRNA sequence.
ACCESSION   AA867755
VERSION     AA867755.1  GI:2963200
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:667151
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1264599"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT        6 a      13 c       9 g       3 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      22 gaccctgctgccc 34
           |||||||||||||
Db      16 GACCCTGCTGCCC 28


RESULT  24
AZ777749/c
LOCUS       AZ777749       31 bp    DNA             GSS       16-FEB-2001
DEFINITION  2M0012H13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0012H13 F, DNA sequence.
ACCESSION   AZ777749
VERSION     AZ777749.1  GI:12906501
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0012  row: H  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0012H13"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        5 a       7 c      12 g       7 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     373 cagccacttgtcc 385
           |||||||||||||
Db      26 CAGCCACTTGTCC 14


RESULT  25
AZ938547/c
LOCUS       AZ938547       31 bp    DNA             GSS       26-APR-2001
DEFINITION  2M0197J10F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0197J10 F, DNA sequence.
ACCESSION   AZ938547
VERSION     AZ938547.1  GI:13798394
```

```
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0197  row: J  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0197J10"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       5 a      2 c     11 g     13 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1513 caaccctgagatt 1525
           |||||||||||||
Db     25 CAACCCTGAGATT 13


RESULT  26
AZ618214
LOCUS       AZ618214       32 bp    DNA             GSS       13-DEC-2000
DEFINITION  1M0449O16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0449O16 R, DNA sequence.
ACCESSION   AZ618214
```

```
VERSION     AZ618214.1  GI:11740404
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0449  row: O  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0449O16"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       5 a      9 c     10 g      8 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1551 tgcagatggactt 1563
           |||||||||||||
Db      5 TGCAGATGGACTT 17


RESULT  27
AA920912
LOCUS       AA920912       34 bp    mRNA            EST       20-APR-1998
DEFINITION  vy84f09.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1312937 5' similar to SW:CB45_MOUSE Q61112 45 KD
```

```
          CALCIUM-BINDING PROTEIN PRECURSOR ;, mRNA sequence.
ACCESSION AA920912
VERSION   AA920912.1  GI:3067691
KEYWORDS  EST.
SOURCE    house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1  (bases 1 to 34)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:683233
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1312937"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT        6 a     14 c      7 g      7 t
ORIGIN
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  Query Match             0.7%;  Score 13;  DB 10;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     695 tccttcaccctga 707
           ||||||||||||
Db       9 TCCTTCACCCTGA 21
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RESULT  28
AZ469734
LOCUS       AZ469734       35 bp    DNA             GSS       04-OCT-2000
DEFINITION  1M0283J19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0283J19 F, DNA sequence.
ACCESSION   AZ469734
VERSION     AZ469734.1  GI:10627859
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0283  row: J  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0283J19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a     24 c      2 g      9 t
ORIGIN
```

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  Query Match             0.7%;  Score 13;  DB 13;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     913 cctccccctcccc 925
           ||||||||||||
Db      23 CCTCCCCCTCCCC 35
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RESULT  29
AZ825411/c
LOCUS       AZ825411       36 bp    DNA             GSS       20-FEB-2001
DEFINITION  2M0100A09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0100A09 R, DNA sequence.
ACCESSION   AZ825411
VERSION     AZ825411.1  GI:12995319
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
```

```
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0100  row: A  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0100A09"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       11 a      7 c      7 g     11 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 13;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1167 ccaagatctcctg 1179
           |||||||||||||
Db     36 CCAAGATCTCCTG 24


RESULT  30
AA978054
LOCUS       AA978054       37 bp    mRNA            EST       23-JUL-1998
DEFINITION  oq55h01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1590289 3'
            similar to SW:KAD2_HUMAN P54819 ADENYLATE KINASE ISOENZYME 2,
            MITOCHONDRIAL ;, mRNA sequence.
ACCESSION   AA978054
VERSION     AA978054.1  GI:3155500
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 419   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1590289"
                     /clone_lib="NCI_CGAP_Kid5"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT        7 a      12 c      9 g      9 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    659 cctgggtggatca 671
          |||||||||||||
Db      6 CCTGGGTGGATCA 18


RESULT  31
AZ663277
LOCUS       AZ663277       39 bp    DNA             GSS       14-DEC-2000
DEFINITION  1M0542O15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0542O15 R, DNA sequence.
ACCESSION   AZ663277
VERSION     AZ663277.1  GI:11800423
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: O column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.

FEATURES Location/Qualifiers
source 1. .39
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542O15"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 7 c 7 g 20 t
ORIGIN

Query Match 0.7%; Score 13; DB 13; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ctcatgttccgtg 55
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Db 10 CTCATGTTCCGTG 22

RESULT 32
AZ781715/c
LOCUS AZ781715 39 bp DNA GSS 16-FEB-2001
DEFINITION 2M0021F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021F16 F, DNA sequence.
ACCESSION AZ781715
VERSION AZ781715.1 GI:12914686
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 39)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0021 row: F column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 39.

FEATURES Location/Qualifiers
source 1. .39
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0021F16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 3 c 17 g 7 t
ORIGIN

Query Match 0.7%; Score 13; DB 13; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 tcctgaccctggc 159
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Db 26 TCCTGACCCTGGC 14

RESULT 33
AZ825536/c
LOCUS AZ825536 39 bp DNA GSS 20-FEB-2001
DEFINITION 2M0100J14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0100J14 R, DNA sequence.
ACCESSION AZ825536
VERSION AZ825536.1 GI:12995444
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 39)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

```
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0100  row: J  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 39.
FEATURES              Location/Qualifiers
     source           1. .39
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0100J14"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        7 a      3 c     21 g      8 t
ORIGIN
```

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  Query Match              0.7%;  Score 13;  DB 13;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    917 cccctccccacct 929
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Db     26 CCCCTCCCCACCT 14
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RESULT  34
AA680336
LOCUS       AA680336       40 bp    mRNA            EST       02-DEC-1997
DEFINITION  ac83e09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
            IMAGE:869224 3' similar to TR:G836930 G836930 MELANOMA ANTIGEN P15.
            ;, mRNA sequence.
ACCESSION   AA680336
VERSION     AA680336.1  GI:2656304
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .40
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:869224"
                      /clone_lib="Stratagene lung (#937210)"
                      /sex="male"
                      /dev_stage="72 years"
                      /lab_host="SOLR cells (kanamycin resistant)"
                      /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
                      ; Site_2: XhoI; Cloned unidirectionally.  Primer: Oligo
                      dT. normal lung.  Average insert size: 1.0 kb; Uni-ZAP XR
                      Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3'
                      adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT        5 a     16 c      9 g     10 t
ORIGIN
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  Query Match              0.7%;  Score 13;  DB 10;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1686 ctcctccagcgtg 1698
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Db     20 CTCCTCCAGCGTG 32
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RESULT  35
AI001093
LOCUS       AI001093       40 bp    mRNA            EST       05-JUN-1998
DEFINITION  os94c01.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612992 3'
            similar to SW:TISD_HUMAN P47974 TIS11D PROTEIN ;, mRNA sequence.
ACCESSION   AI001093
VERSION     AI001093.1  GI:3191647
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .40
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
```

```
                     /clone="IMAGE:1612992"
                     /clone_lib="NCI_CGAP_GC3"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is not normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        4 a      13 c      20 g       3 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      55 gggggctgggcgg 67
           |||||||||||||
Db       4 GGGGGCTGGGCGG 16


RESULT  36
BE383987/c
LOCUS       BE383987       42 bp    mRNA            EST       21-JUL-2000
DEFINITION  601273364F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614462 5',
            mRNA sequence.
ACCESSION   BE383987
VERSION     BE383987.1  GI:9329352
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM276  row: p  column: 15
            High quality sequence start: 27
            High quality sequence stop: 42.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3614462"
                     /clone_lib="NIH_MGC_20"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        9 a       5 c      17 g      11 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     852 cagcctcctacct 864
           |||||||||||||
Db      20 CAGCCTCCTACCT 8


RESULT  37
AA922988
LOCUS       AA922988       44 bp    mRNA            EST       21-APR-1998
DEFINITION  ok77f09.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1520009 3'
            similar to gb:S41211 HOMEOBOX PROTEIN HOX-A10 (HUMAN);, mRNA
            sequence.
ACCESSION   AA922988
VERSION     AA922988.1  GI:3070297
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1520009"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        7 a       8 c      15 g      14 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1541 ttcctgctgctgc 1553
           |||||||||||||
Db      26 TTCCTGCTGCTGC 38


RESULT  38
T48887
LOCUS       T48887         44 bp    mRNA            EST       06-FEB-1995
DEFINITION  yb07a05.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone
```

IMAGE:70448 5' similar to similar to gb:X14088 EOSINOPHIL GRANULE MAJOR BASIC PROTEIN PRECURSOR (HUMAN), mRNA sequence.
ACCESSION T48887
VERSION T48887.1 GI:650747
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 44)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High qality sequence starts: 1
High qality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: M13RP1
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .44
/organism="Homo sapiens"
/db_xref="GDB:491345"
/db_xref="taxon:9606"
/clone="IMAGE:70448"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 12 a 8 c 14 g 9 t 1 others
ORIGIN

Query Match 0.7%; Score 13; DB 11; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1427 gtgggcatccctg 1439
|||||||||||||
Db 30 GTGGGCATCCCTG 42

RESULT 39
AZ498888/c
LOCUS AZ498888 44 bp DNA GSS 05-OCT-2000
DEFINITION 1M0336E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0336E21 F, DNA sequence.
ACCESSION AZ498888
VERSION AZ498888.1 GI:10677165
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 44)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0336 row: E column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 44.

FEATURES Location/Qualifiers
source 1. .44
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0336E21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 15 c 18 g 8 t
ORIGIN

Query Match 0.7%; Score 13; DB 13; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 cgggcgagaaggc 324
|||||||||||||
Db 40 CGGGCGAGAAGGC 28

RESULT 40
AZ480635/c
LOCUS AZ480635 45 bp DNA GSS 04-OCT-2000
DEFINITION 1M0302M18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0302M18 F, DNA sequence.
ACCESSION AZ480635
VERSION AZ480635.1 GI:10641700
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0302  row: M  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0302M18"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       10 a      12 c      12 g      11 t
ORIGIN
```

```
  Query Match             0.7%;  Score 13;  DB 13;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     113 caccactgcctga 125
           ||||||||||||
Db      19 CACCACTGCCTGA 7
```

```
RESULT  41
AA730149
LOCUS       AA730149        46 bp    mRNA            EST       22-JAN-1998
DEFINITION  nx38f03.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1258397 3'
            similar to TR:Q99544 Q99544 M-PHASE PHOSPHOPROTEIN 4 ;contains Alu
            repetitive element;, mRNA sequence.
ACCESSION   AA730149
VERSION     AA730149.1  GI:2751431
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 704   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1258397"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       14 a      11 c       9 g      12 t
ORIGIN
```

```
  Query Match             0.7%;  Score 13;  DB 10;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     874 tcacaagggtcat 886
           ||||||||||||||
Db      24 TCACAAGGGTCAT 36
```

```
RESULT  42
AA902889
LOCUS       AA902889        46 bp    mRNA            EST       09-JUN-1998
DEFINITION  oj49g04.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1501686 3'
            similar to TR:Q29294 Q29294 ZINC FINGER PROTEIN ;, mRNA sequence.
ACCESSION   AA902889
VERSION     AA902889.1  GI:3038012
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
```

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1180 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1501686"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 11 a 19 c 13 g 3 t
ORIGIN

Query Match 0.7%; Score 13; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 310 cacgggcgagaag 322
||||||||||||
Db 31 CACGGGCGAGAAG 43

RESULT 43
AI026096
LOCUS AI026096 46 bp mRNA EST 27-AUG-1998
DEFINITION ov94h09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645025 3' similar to TR:Q62006 Q62006 OPA REPEAT ;contains element L1 repetitive element ;, mRNA sequence.
ACCESSION AI026096
VERSION AI026096.1 GI:3241709
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1791 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1645025"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 7 a 6 c 18 g 15 t
ORIGIN

Query Match 0.7%; Score 13; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 gtggctgggtatt 508
||||||||||||
Db 10 GTGGCTGGGTATT 22

RESULT 44
AI264859
LOCUS AI264859 46 bp mRNA EST 03-FEB-1999
DEFINITION qx66h12.x1 NCI_CGAP_Ov36 Homo sapiens cDNA clone IMAGE:2006375 3' similar to SW:NHPX_HUMAN P55769 NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG ;, mRNA sequence.
ACCESSION AI264859
VERSION AI264859.1 GI:3873062
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 200 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2006375"
/clone_lib="NCI_CGAP_Ov36"
/sex="female"
/tissue_type="borderline ovarian carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP1; mRNA made from borderline ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. "

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BASE COUNT       10 a     12 c     12 g     12 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1156 cctcaagatgccc 1168
          |||||||||||||
Db     14 CCTCAAGATGCCC 26


RESULT  45
AI439347/c
LOCUS       AI439347       46 bp    mRNA            EST       30-MAR-1999
DEFINITION  ti54f06.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134307 3'
            similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;, mRNA sequence.
ACCESSION   AI439347
VERSION     AI439347.1  GI:4303686
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11547-015
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1143    Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2134307"
                     /clone_lib="NCI_CGAP_Lym12"
                     /tissue_type="lymphoma, follicular mixed small and large
                     cell"
                     /lab_host="DH10B"
                     /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT.  Average insert size 1.25 kb. Life Technologies
                     catalog #: 11547-015"
BASE COUNT       18 a      8 c      7 g     13 t
ORIGIN


  Query Match             0.7%;  Score 13;  DB 10;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1258 agcttacacattt 1270
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Db     29 AGCTTACACATTT 17


Search completed: April 20, 2002, 00:25:44
Job time: 9048 sec
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